



46

24751-2502

SEQUENCE LISTING

<110> Jensen, Michael

<120> Selection Systems for Genetically
Modified Cells

<130> 24751-2502

<140> US/09/846,637

<141> 2001-04-30

<160> 39

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1654

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (48)...(1589)

<223> Human Wild-type Inosine Monophospate Dehydrogenase
II (IMPDH II)

<300>

<301> Collart, F.R. and Huberman, E.

<302> Cloning and sequence analysis of the human and

<303> J. Biol. Chem. (1988)

<304> 263

<306> 15769-15772

<400> 1

gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac 56
Met Ala Asp
1

tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca 104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
5 10 15

gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt 152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
20 25 30 35

ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg 200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
40 45 50

act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc 248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
55 60 65

tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg 296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
70 75 80

ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc 344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
85 90 95

cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc 392

Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln	Gly	Phe	Ile	
100					105					110					115	
aca	gac	cct	gtg	gtc	ctc	agc	ccc	aag	gat	cgc	gtg	cgg	gat	gtt	ttt	440
Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg	Asp	Val	Phe	
				120					125					130		
gag	gcc	aag	gcc	cgg	cat	ggt	ttc	tgc	ggt	atc	cca	atc	aca	gac	aca	488
Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile	Thr	Asp	Thr	
			135					140					145			
ggc	cgg	atg	ggg	agc	cgc	ttg	gtg	ggc	atc	atc	tcc	tcc	agg	gac	att	536
Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser	Arg	Asp	Ile	
		150					155					160				
gat	ttt	ctc	aaa	gag	gag	gaa	cat	gac	tgt	ttc	ttg	gaa	gag	ata	atg	584
Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Cys	Phe	Leu	Glu	Glu	Ile	Met	
	165					170					175					
aca	aag	agg	gaa	gac	ttg	gtg	gta	gcc	ccc	cgc	agc	atc	aca	ctg	aag	632
Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Arg	Ser	Ile	Thr	Leu	Lys	
					185					190					195	
gag	gca	aat	gaa	att	ctg	cag	cgc	agc	aag	aag	gga	aag	ttg	ccc	att	680
Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys	Leu	Pro	Ile	
				200					205					210		
gta	aat	gaa	gat	gat	gag	ctt	gtg	gcc	atc	att	gcc	cgg	aca	gac	ctg	728
Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg	Thr	Asp	Leu	
			215					220					225			
aag	aag	aat	cgg	gac	tac	cca	cta	gcc	tcc	aaa	gat	gcc	aag	aaa	cag	776
Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala	Lys	Lys	Gln	
		230					235					240				
ctg	ctg	tgt	ggg	gca	gcc	att	ggc	act	cat	gag	gat	gac	aag	tat	agg	824
Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp	Lys	Tyr	Arg	
	245					250					255					
ctg	gac	ttg	ctc	gcc	cag	gct	ggc	gtg	gat	gta	gtg	gtt	ttg	gac	tct	872
Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val	Leu	Asp	Ser	
	260				265					270					275	
tcc	cag	gga	aat	tcc	atc	ttc	cag	atc	aat	atg	atc	aag	tac	atc	aaa	920
Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys	Tyr	Ile	Lys	
				280					285					290		
gac	aaa	tac	cct	aat	ctc	caa	gtc	att	gga	ggc	aat	gtg	gtc	act	gct	968
Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	Val	Thr	Ala	
			295					300					305			
gcc	cag	gcc	aag	aac	ctc	att	gat	gca	ggt	gtg	gat	gcc	ctg	cgg	gtg	1016
Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala	Leu	Arg	Val	
		310					315					320				
ggc	atg	gga	agt	ggc	tcc	atc	tgc	att	acg	cag	gaa	gtg	ctg	gcc	tgt	1064
Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	Leu	Ala	Cys	
	325					330					335					
ggg	cgg	ccc	caa	gca	aca	gca	gtg	tac	aag	gtg	tca	gag	tat	gca	cgg	1112
Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu	Tyr	Ala	Arg	
	340				345					350					355	
cgc	ttt	ggt	gtt	ccg	gtc	att	gct	gat	gga	gga	atc	caa	aat	gtg	ggt	1160
Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln	Asn	Val	Gly	

360								365								370								
cat	att	gcg	aaa	gcc	ttg	gcc	ctt	ggg	gcc	tcc	aca	gtc	atg	atg	ggc	1208								
His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	Met	Met	Gly									
			375					380					385											
tct	ctc	ctg	gct	gcc	acc	act	gag	gcc	cct	ggg	gaa	tac	ttc	ttt	tcc	1256								
Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	Phe	Phe	Ser									
		390					395					400												
gat	ggg	atc	cgg	cta	aag	aaa	tat	cgc	ggg	atg	ggg	tct	ctc	gat	gcc	1304								
Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser	Leu	Asp	Ala									
	405					410					415													
atg	gac	aag	cac	ctc	agc	agc	cag	aac	aga	tat	ttc	agt	gaa	gct	gac	1352								
Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser	Glu	Ala	Asp									
	420				425					430					435									
aaa	atc	aaa	gtg	gcc	cag	gga	gtg	tct	ggg	gct	gtg	cag	gac	aaa	ggg	1400								
Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln	Asp	Lys	Gly									
			440						445				450											
tca	atc	cac	aaa	ttt	gtc	cct	tac	ctg	att	gct	ggc	atc	caa	cac	tca	1448								
Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile	Gln	His	Ser									
			455					460					465											
tgc	cag	gac	att	ggg	gcc	aag	agc	ttg	acc	caa	gtc	cga	gcc	atg	atg	1496								
Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg	Ala	Met	Met									
		470					475					480												
tac	tct	ggg	gag	ctt	aag	ttt	gag	aag	aga	acg	tcc	tca	gcc	cag	gtg	1544								
Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser	Ala	Gln	Val									
	485					490					495													
gaa	ggg	ggc	gtc	cat	agc	ctc	cat	tcg	tat	gag	aag	cgg	ctt	ttc		1589								
Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg	Leu	Phe										
	500				505				510															
tgaaaaggga	tccagcacac	ctcctcggtt	tttttttcaa	taaaagttta	gaaagacccg	1649																		
aattc						1654																		

<210> 2
 <211> 514
 <212> PRT
 <213> Homo sapien

<400> 2

Met	Ala	Asp	Tyr	Leu	Ile	Ser	Gly	Gly	Thr	Ser	Tyr	Val	Pro	Asp	Asp
1				5					10					15	
Gly	Leu	Thr	Ala	Gln	Gln	Leu	Phe	Asn	Cys	Gly	Asp	Gly	Leu	Thr	Tyr
			20					25					30		
Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Tyr	Ile	Asp	Phe	Thr	Ala	Asp	Gln
		35					40					45			
Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys	Thr	Pro
	50					55					60				
Leu	Val	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	Ala	Ile
	65				70					75					80
Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr
			85					90					95		
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln
			100					105					110		
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg
		115					120					125			
Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile
	130					135					140				

Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser
145					150					155					160
Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Cys	Phe	Leu	Glu
				165					170						175
Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Arg	Ser	Ile
			180					185						190	
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys
		195					200					205			
Leu	Pro	Ile	Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg
	210					215					220				
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala
225					230					235					240
Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp
				245					250					255	
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val
			260					265					270		
Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys
		275					280					285			
Tyr	Ile	Lys	Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val
	290					295					300				
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala
305					310					315					320
Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val
				325					330					335	
Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu
			340					345					350		
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln
		355					360					365			
Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val
	370					375					380				
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr
385					390					395					400
Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser
				405					410					415	
Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser
			420					425					430		
Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln
		435					440					445			
Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile
	450					455					460				
Gln	His	Ser	Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg
465					470					475					480
Ala	Met	Met	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser
				485					490					495	
Ala	Gln	Val	Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg
			500					505					510		
Leu	Phe														

<210> 3

<211> 1654

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (48)...(1589)

<223> T333I/S351Y Human IMPDH II mutant

<221> mutation

<222> 1045

<223> C to T mutation

<221> mutation

<222> 1046

<223> G to C mutation

<221> mutation

<222> 1099

<223> C to A mutation

<221> mutation

<222> 1100

<223> A to T mutation

<400> 3

gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac 56
Met Ala Asp
1

tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca 104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
5 10 15

gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt 152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe
20 25 30 35

ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg 200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu
40 45 50

act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc 248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser
55 60 65

tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg 296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala
70 75 80

ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc 344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe
85 90 95

cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc 392
Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile
100 105 110 115

aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt 440
Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe
120 125 130

gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca 488
Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr
135 140 145

ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att 536
Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile
150 155 160

gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg 584
Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met
165 170 175

aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag 632
Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile Thr Leu Lys
180 185 190 195

gag gca aat gaa att ctg cag cgc agc aag aag gga aag ttg ccc att 680
Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu Pro Ile

200				205				210								
gta	aat	gaa	gat	gat	gag	ctt	gtg	gcc	atc	att	gcc	cgg	aca	gac	ctg	728
Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg	Thr	Asp	Leu	
			215					220					225			
aag	aag	aat	cgg	gac	tac	cca	cta	gcc	tcc	aaa	gat	gcc	aag	aaa	cag	776
Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala	Lys	Lys	Gln	
		230					235					240				
ctg	ctg	tgt	ggg	gca	gcc	att	ggc	act	cat	gag	gat	gac	aag	tat	agg	824
Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp	Lys	Tyr	Arg	
	245					250					255					
ctg	gac	ttg	ctc	gcc	cag	gct	ggg	gtg	gat	gta	gtg	gtt	ttg	gac	tct	872
Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val	Leu	Asp	Ser	
260					265					270					275	
tcc	cag	gga	aat	tcc	atc	ttc	cag	atc	aat	atg	atc	aag	tac	atc	aaa	920
Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys	Tyr	Ile	Lys	
			280					285					290			
gac	aaa	tac	cct	aat	ctc	caa	gtc	att	gga	ggc	aat	gtg	gtc	act	gct	968
Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	Val	Thr	Ala	
			295					300					305			
gcc	cag	gcc	aag	aac	ctc	att	gat	gca	ggg	gtg	gat	gcc	ctg	cgg	gtg	1016
Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala	Leu	Arg	Val	
		310					315					320				
ggc	atg	gga	agt	ggc	tcc	atc	tgc	att	atc	cag	gaa	gtg	ctg	gcc	tgt	1064
Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Ile	Gln	Glu	Val	Leu	Ala	Cys	
	325					330					335					
ggg	cgg	ccc	caa	gca	aca	gca	gtg	tac	aag	gtg	tat	gag	tat	gca	cgg	1112
Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Tyr	Glu	Tyr	Ala	Arg	
340					345					350					355	
cgc	ttt	ggg	gtt	ccg	gtc	att	gct	gat	gga	gga	atc	caa	aat	gtg	ggg	1160
Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln	Asn	Val	Gly	
				360					365					370		
cat	att	gcg	aaa	gcc	ttg	gcc	ctt	ggg	gcc	tcc	aca	gtc	atg	atg	ggc	1208
His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	Met	Met	Gly	
			375					380					385			
tct	ctc	ctg	gct	gcc	acc	act	gag	gcc	cct	ggg	gaa	tac	ttc	ttt	tcc	1256
Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	Phe	Phe	Ser	
		390					395					400				
gat	ggg	atc	cgg	cta	aag	aaa	tat	cgc	ggg	atg	ggg	tct	ctc	gat	gcc	1304
Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser	Leu	Asp	Ala	
	405					410					415					
atg	gac	aag	cac	ctc	agc	agc	cag	aac	aga	tat	ttc	agt	gaa	gct	gac	1352
Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser	Glu	Ala	Asp	
420					425				430						435	
aaa	atc	aaa	gtg	gcc	cag	gga	gtg	tct	ggg	gct	gtg	cag	gac	aaa	ggg	1400
Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln	Asp	Lys	Gly	
				440					445					450		
tca	atc	cac	aaa	ttt	gtc	cct	tac	ctg	att	gct	ggc	atc	caa	cac	tca	1448
Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile	Gln	His	Ser	
			455					460					465			

tgc cag gac att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg 1496
 Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met
 470 475 480

tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg 1544
 Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val
 485 490 495

gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc 1589
 Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
 500 505 510

tgaaaaggga tccagcacac ctcctcggtt tttttttcaa taaaagtta gaaagaccg 1649
 aattc 1654

<210> 4
 <211> 514
 <212> PRT
 <213> Homo sapien

<400> 4
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
 1 5 10 15
 Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
 20 25 30
 Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35 40 45
 Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50 55 60
 Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
 65 70 75 80
 Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95
 Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
 100 105 110
 Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
 115 120 125
 Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
 130 135 140
 Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
 145 150 155 160
 Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
 165 170 175
 Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile
 180 185 190
 Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
 195 200 205
 Leu Pro Ile Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg
 210 215 220
 Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
 225 230 235 240
 Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
 245 250 255
 Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val
 260 265 270
 Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
 275 280 285
 Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
 290 295 300
 Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
 305 310 315 320
 Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Ile Gln Glu Val
 325 330 335
 Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Tyr Glu

<400> 5																
gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac																56
Met Ala Asp																
1																
tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca																104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr																
5 10 15																
gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt																152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe																
20 25 30 35																
ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg																200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu																
40 45 50																
act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc																248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser																
55 60 65																

tct	ccc	atg	gac	aca	gtc	aca	gag	gct	ggg	atg	gcc	ata	gca	atg	gcg	296
Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	Ala	Ile	Ala	Met	Ala	
		70					75					80				
ctt	aca	ggc	ggg	att	ggc	ttc	atc	cac	cac	aac	tgt	aca	cct	gaa	ttc	344
Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr	Pro	Glu	Phe	
	85					90					95					
cag	gcc	aat	gaa	gtt	cgg	aaa	gtg	aag	aaa	tat	gaa	cag	gga	ttc	atc	392
Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln	Gly	Phe	Ile	
100					105					110					115	
aca	gac	cct	gtg	gtc	ctc	agc	ccc	aag	gat	cgc	gtg	cgg	gat	gtt	ttt	440
Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg	Asp	Val	Phe	
				120					125					130		
gag	gcc	aag	gcc	cgg	cat	ggg	ttc	tgc	ggg	atc	cca	atc	aca	gac	aca	488
Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile	Thr	Asp	Thr	
			135					140					145			
ggc	cgg	atg	ggg	agc	cgc	ttg	gtg	ggc	atc	atc	tcc	tcc	agg	gac	att	536
Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser	Arg	Asp	Ile	
		150					155					160				
gat	ttt	ctc	aaa	gag	gag	gaa	cat	gac	tgt	ttc	ttg	gaa	gag	ata	atg	584
Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Cys	Phe	Leu	Glu	Glu	Ile	Met	
	165					170					175					
aca	aag	agg	gaa	gac	ttg	gtg	gta	gcc	ccc	cgc	agc	atc	aca	ctg	aag	632
Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Arg	Ser	Ile	Thr	Leu	Lys	
180					185					190					195	
gag	gca	aat	gaa	att	ctg	cag	cgc	agc	aag	aag	gga	aag	ttg	ccc	att	680
Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys	Leu	Pro	Ile	
				200					205					210		
gta	aat	gaa	gat	gat	gag	ctt	gtg	gcc	atc	att	gcc	cgg	aca	gac	ctg	728
Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg	Thr	Asp	Leu	
			215					220					225			
aag	aag	aat	cgg	gac	tac	cca	cta	gcc	tcc	aaa	gat	gcc	aag	aaa	cag	776
Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala	Lys	Lys	Gln	
		230					235					240				
ctg	ctg	tgt	ggg	gca	gcc	att	ggc	act	cat	gag	gat	gac	aag	tat	agg	824
Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp	Lys	Tyr	Arg	
	245					250					255					
ctg	gac	ttg	ctc	gcc	cag	gct	ggg	gtg	gat	gta	gtg	gtt	ttg	gac	tct	872
Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val	Leu	Asp	Ser	
260					265					270					275	
tcc	cgg	gga	aat	tcc	atc	ttc	cag	atc	aat	atg	atc	aag	tac	atc	aaa	920
Ser	Arg	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys	Tyr	Ile	Lys	
				280					285					290		
gac	aaa	tac	cct	aat	ctc	caa	gtc	att	gga	ggc	aat	gtg	gtc	act	gct	968
Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	Val	Thr	Ala	
			295					300					305			
gcc	cag	gcc	aag	aac	ctc	att	gat	gca	ggg	gtg	gat	gcc	ctg	cgg	gtg	1016
Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala	Leu	Arg	Val	
		310					315					320				

ggc atg gga agt ggc tcc atc tgc att acg cag gaa gtg ctg gcc tgt 1064
 Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys
 325 330 335

ggg cgg ccc caa gca aca gca gtg tac aag gtg tca gag tat gca cgg 1112
 Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr Ala Arg
 340 345 350 355

cgc ttt ggt gtt ccg gtc att gct gat gga gga atc caa aat gtg ggt 1160
 Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val Gly
 360 365 370

cat att gcg aaa gcc ttg gcc ctt ggg gcc tcc aca gtc atg atg ggc 1208
 His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met Gly
 375 380 385

tct ctc ctg gct gcc acc act gag gcc cct ggt gaa tac ttc ttt tcc 1256
 Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe Ser
 390 395 400

gat ggg atc cgg cta aag aaa tat cgc ggt atg ggt tct ctc gat gcc 1304
 Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu Asp Ala
 405 410 415

atg gac aag cac ctc agc agc cag aac aga tat ttc agt gaa gct gac 1352
 Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp
 420 425 430 435

aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac aaa ggg 1400
 Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys Gly
 440 445 450

tca atc cac aaa ttt gtc cct tac ctg att gct ggc atc caa cac tca 1448
 Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln His Ser
 455 460 465

tgc cag gac att ggt gcc aag agc ttg acc caa gtc cga gcc atg atg 1496
 Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met Met
 470 475 480

tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc cag gtg 1544
 Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln Val
 485 490 495

gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt ttc 1589
 Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
 500 505 510

tgaaaaggga tccagcacac ctccctcggtt tttttttcaa taaaagttta gaaagacccg 1649
 aattc 1654

<210> 6
 <211> 514
 <212> PRT
 <213> Homo sapien

<400> 6
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
 1 5 10 15
 Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
 20 25 30
 Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35 40 45
 Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50 55 60

Leu	Val	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	Ala	Ile
65					70					75					80
Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr
				85					90					95	
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln
			100					105					110		
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg
		115					120					125			
Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile
	130					135					140				
Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser
145					150					155					160
Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Cys	Phe	Leu	Glu
				165				170						175	
Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Arg	Ser	Ile
			180					185					190		
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys
		195					200					205			
Leu	Pro	Ile	Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg
	210					215					220				
<hr/>															
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala
225					230					235					240
Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp
				245					250					255	
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val
			260					265					270		
Leu	Asp	Ser	Ser	Arg	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys
		275					280					285			
Tyr	Ile	Lys	Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val
	290					295					300				
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala
305					310					315					320
Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val
				325					330					335	
Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu
			340					345					350		
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln
		355					360					365			
Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val
	370					375					380				
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr
385					390					395					400
Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser
				405					410					415	
Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser
			420					425					430		
Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln
		435					440					445			
Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile
	450					455					460				
Gln	His	Ser	Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg
465					470					475					480
Ala	Met	Met	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser
				485					490					495	
Ala	Gln	Val	Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg
			500					505					510		
Leu	Phe														

<210> 7
 <211> 1654
 <212> DNA
 <213> Homo sapien

<220>

<221> mutation
 <222> 1431
 <223> G to A mutation

<221> CDS
 <222> (48)...(1589)
 <223> Ala462Thr Human IMPDH II mutant

<300>
 <301> Farazi et al.
 <303> J. Biol. Chem. (1997)
 <304> 272
 <305> 2
 <306> 961-965

<400> 7
 gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac 56
 Met Ala Asp
 1

tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca	104
Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr	
5 10 15	
gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt	152
Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn Asp Phe	
20 25 30 35	
ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg gac ctg	200
Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val Asp Leu	
40 45 50	
act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg gtt tcc	248
Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu Val Ser	
55 60 65	
tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca atg gcg	296
Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala Met Ala	
70 75 80	
ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct gaa ttc	344
Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro Glu Phe	
85 90 95	
cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga ttc atc	392
Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly Phe Ile	
100 105 110 115	
aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt	440
Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe	
120 125 130	
gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca gac aca	488
Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr Asp Thr	
135 140 145	
ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg gac att	536
Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg Asp Ile	
150 155 160	
gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag ata atg	584
Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu Glu Ile Met	
165 170 175	
aca aag agg gaa gac ttg gtg gta gcc ccc cgc agc atc aca ctg aag	632

Thr 180	Lys	Arg	Glu	Asp	Leu 185	Val	Val	Ala	Pro	Arg 190	Ser	Ile	Thr	Leu	Lys 195	
gag Glu	gca Ala	aat Asn	gaa Glu	att Ile 200	ctg Leu	cag Gln	cgc Arg	agc Ser	aag Lys 205	aag Lys	gga Gly	aag Lys	ttg Leu	ccc Pro 210	att Ile	680
gta Val	aat Asn	gaa Glu	gat Asp 215	gat Asp	gag Glu	ctt Leu	gtg Val	gcc Ala 220	atc Ile	att Ile	gcc Ala	cgg Arg	aca Thr 225	gac Asp	ctg Leu	728
aag Lys	aag Lys	aat Asn 230	cgg Arg	gac Asp	tac Tyr	cca Pro	cta Leu 235	gcc Ala	tcc Ser	aaa Lys	gat Asp	gcc Ala 240	aag Lys	aaa Lys	cag Gln	776
ctg Leu 245	ctg Leu	tgt Cys	ggg Gly	gca Ala	gcc Ala	att Ile 250	ggc Gly	act Thr	cat His	gag Glu	gat Asp 255	gac Asp	aag Lys	tat Tyr	agg Arg	824
ctg Leu 260	gac Asp	ttg Leu	ctc Leu	gcc Ala	cag Gln 265	gct Ala	ggc Gly	gtg Val	gat Asp	gta Val 270	gtg Val	gtt Val	ttg Leu	gac Asp	tct Ser 275	872
tcc Ser	cag Gln	gga Gly	aat Asn	tcc Ser 280	atc Ile	ttc Phe	cag Gln	atc Ile	aat Asn 285	atg Met	atc Ile	aag Lys	tac Tyr	atc Ile 290	aaa Lys	920
gac Asp	aaa Lys	tac Tyr	cct Pro 295	aat Asn	ctc Leu	caa Gln	gtc Val	att Ile 300	gga Gly	ggc Gly	aat Asn	gtg Val 305	gtc Val	act Thr	gct Ala	968
gcc Ala	cag Gln	gcc Ala 310	aag Lys	aac Asn	ctc Leu	att Ile	gat Asp 315	gca Ala	ggc Gly	gtg Val	gat Asp	gcc Ala 320	ctg Leu	cgg Arg	gtg Val	1016
ggc Gly 325	atg Met	gga Gly	agt Ser	ggc Gly	tcc Ser	atc Ile 330	tgc Cys	att Ile	acg Thr	cag Gln	gaa Glu 335	gtg Val	ctg Leu	gcc Ala	tgt Cys	1064
ggg Gly 340	cgg Arg	ccc Pro	caa Gln	gca Ala	aca Thr 345	gca Ala	gtg Val	tac Tyr	aag Lys	gtg Val 350	tca Ser	gag Glu	tat Tyr	gca Ala	cgg Arg 355	1112
cgc Arg	ttt Phe	ggc Gly	gtt Val	ccg Pro 360	gtc Val	att Ile	gct Ala	gat Asp	gga Gly 365	gga Gly	atc Ile	caa Gln	aat Asn	gtg Val 370	ggc Gly	1160
cat His	att Ile	gcg Ala	aaa Lys 375	gcc Ala	ttg Leu	gcc Ala	ctt Leu	ggg Gly 380	gcc Ala	tcc Ser	aca Thr	gtc Val	atg Met 385	atg Met	ggc Gly	1208
tct Ser	ctc Leu	ctg Leu 390	gct Ala	gcc Ala	acc Thr	act Thr	gag Glu 395	gcc Ala	cct Pro	ggc Gly	gaa Glu	tac Tyr 400	ttc Phe	ttt Phe	tcc Ser	1256
gat Asp 405	ggg Gly	atc Ile	cgg Arg	cta Leu	aag Lys	aaa Lys 410	tat Tyr	cgc Arg	ggc Gly	atg Met	ggc Gly 415	tct Ser	ctc Leu	gat Asp	gcc Ala	1304
atg Met 420	gac Asp	aag Lys	cac His	ctc Leu	agc Ser 425	agc Ser	cag Gln	aac Asn	aga Arg	tat Tyr 430	ttc Phe	agt Ser	gaa Glu	gct Ala	gac Asp 435	1352
aaa Lys	atc Ile	aaa Lys	gtg Val	gcc Ala	cag Gln	gga Gly	gtg Val	tct Ser	ggc Gly	gct Ala	gtg Val	cag Gln	gac Asp	aaa Lys	ggg Gly	1400

440								445				450				
tca	atc	cac	aaa	ttt	gtc	cct	tac	ctg	att	act	ggc	atc	caa	cac	tca	1448
Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Thr	Gly	Ile	Gln	His	Ser	
			455					460					465			
tgc	cag	gac	att	ggg	gcc	aag	agc	ttg	acc	caa	gtc	cga	gcc	atg	atg	1496
Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg	Ala	Met	Met	
		470					475					480				
tac	tct	ggg	gag	ctt	aag	ttt	gag	aag	aga	acg	tcc	tca	gcc	cag	gtg	1544
Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser	Ala	Gln	Val	
	485					490					495					
gaa	ggg	ggc	gtc	cat	agc	ctc	cat	tcg	tat	gag	aag	cgg	ctt	ttc		1589
Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg	Leu	Phe		
500					505				510							
tgaaaaggga tccagcacac ctccctcggtt tttttttcaa taaaagttta gaaagaccgc																
aattc																

<210> 8
 <211> 514
 <212> PRT
 <213> Homo sapien

<400> 8
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
 1 5 10 15
 Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
 20 25 30
 Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35 40 45
 Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50 55 60
 Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
 65 70 75 80
 Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95
 Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
 100 105 110
 Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
 115 120 125
 Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
 130 135 140
 Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
 145 150 155 160
 Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
 165 170 175
 Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile
 180 185 190
 Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
 195 200 205
 Leu Pro Ile Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg
 210 215 220
 Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
 225 230 235 240
 Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
 245 250 255
 Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val
 260 265 270
 Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
 275 280 285
 Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
 290 295 300

```

Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
305          310          315          320
Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val
          325          330          335
Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
          340          345          350
Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
          355          360          365
Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
          370          375          380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385          390          395          400
Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
          405          410          415
Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
          420          425          430
Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
          435          440          445
Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Thr Gly Ile
          450          455          460
Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
465          470          475          480
Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
          485          490          495
Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
          500          505          510
Leu Phe

```

<210> 9
 <211> 1654
 <212> DNA
 <213> Homo sapien

<220>
 <221> mutation
 <222> 877
 <223> A to G mutation

<221> mutation
 <222> 1431
 <223> G to A mutation

<221> CDS
 <222> (48)...(1589)
 <223> Gln277Arg/Ala462Thr Human IMPDH II mutant

<300>
 <301> Farazi et al.
 <302> Isolation and Characterization of Mycophenolic
 <303> J. Biol. Chem. (1997)
 <304> 272
 <305> 2
 <306> 961-965

<400> 9
 gaattcgggc ggtcctcgga gacacgcggc ggtgtcctgt gttggcc atg gcc gac 56
 Met Ala Asp
 1

tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga ctc aca 104
 Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly Leu Thr
 5 10 15

gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat gac ttt 152

Ala 20	Gln	Gln	Leu	Phe	Asn 25	Cys	Gly	Asp	Gly	Leu 30	Thr	Tyr	Asn	Asp	Phe 35	
ctc Leu	att Ile	ctc Leu	cct Pro	ggg Gly 40	tac Tyr	atc Ile	gac Asp	ttc Phe	act Thr 45	gca Ala	gac Asp	cag Gln	gtg Val	gac Asp 50	ctg Leu	200
act Thr	tct Ser	gct Ala	ctg Leu 55	acc Thr	aag Lys	aaa Lys	atc Ile	act Thr 60	ctt Leu	aag Lys	acc Thr	cca Pro	ctg Leu 65	gtt Val	tcc Ser	248
tct Ser	ccc Pro	atg Met 70	gac Asp	aca Thr	gtc Val	aca Thr	gag Glu 75	gct Ala	ggg Gly	atg Met	gcc Ala	ata Ile 80	gca Ala	atg Met	gcg Ala	296
ctt Leu	aca Thr 85	ggc Gly	ggt Gly	att Ile	ggc Gly	ttc Phe 90	atc Ile	cac His	cac His	aac Asn 95	tgt Cys	aca Thr	cct Pro	gaa Glu	ttc Phe	344
cag Gln 100	gcc Ala	aat Asn	gaa Glu	gtt Val	cgg Arg 105	aaa Lys	gtg Val	aag Lys	aaa Lys	tat Tyr 110	gaa Glu	cag Gln	gga Gly	ttc Phe	atc Ile 115	392
aca Thr	gac Asp	cct Pro	gtg Val 120	gtc Val	ctc Leu	agc Ser	ccc Pro	aag Lys	gat Asp 125	cgc Arg	gtg Val	cgg Arg	gat Asp 130	gtt Val	ttt Phe	440
gag Glu	gcc Ala	aag Lys	gcc Ala 135	cgg Arg	cat His	ggt Gly	ttc Phe	tgc Cys 140	ggt Gly	atc Ile	cca Pro	atc Ile	aca Thr 145	gac Asp	aca Thr	488
ggc Gly	cgg Arg	atg Met 150	ggg Gly	agc Ser	cgc Arg	ttg Leu	gtg Val 155	ggc Gly	atc Ile	atc Ile	tcc Ser 160	tcc Ser	agg Arg	gac Asp	att Ile	536
gat Asp 165	ttt Phe	ctc Leu	aaa Lys	gag Glu	gag Glu	gaa Glu 170	cat His	gac Asp	tgt Cys	ttc Phe	ttg Leu 175	gaa Glu	gag Glu	ata Ile	atg Met	584
aca Thr 180	aag Lys	agg Arg	gaa Glu	gac Asp	ttg Leu 185	gtg Val	gta Val	gcc Ala	ccc Pro	cgc Arg 190	agc Ser	atc Ile	aca Thr	ctg Leu 195	aag Lys	632
gag Glu	gca Ala	aat Asn	gaa Glu 200	att Ile	ctg Leu	cag Gln	cgc Arg	agc Ser	aag Lys 205	aag Lys	gga Gly	aag Lys	ttg Leu 210	ccc Pro	att Ile	680
gta Val	aat Asn	gaa Glu 215	gat Asp	gat Asp	gag Glu	ctt Leu	gtg Val	gcc Ala 220	atc Ile	att Ile	gcc Ala	cgg Arg 225	aca Thr	gac Asp	ctg Leu	728
aag Lys	aag Lys	aat Asn 230	cgg Arg	gac Asp	tac Tyr	cca Pro	cta Leu 235	gcc Ala	tcc Ser	aaa Lys	gat Asp	gcc Ala 240	aag Lys	aaa Lys	cag Gln	776
ctg Leu 245	ctg Leu	tgt Cys	ggg Gly	gca Ala	gcc Ala	att Ile 250	ggc Gly	act Thr	cat His	gag Glu	gat Asp 255	gac Asp	aag Lys	tat Tyr	agg Arg	824
ctg Leu 260	gac Asp	ttg Leu	ctc Leu	gcc Ala	cag Gln 265	gct Ala	ggt Gly	gtg Val	gat Asp	gta Val 270	gtg Val	gtt Val	ttg Leu	gac Asp	tct Ser 275	872
tcc Ser	cgg Arg	gga Gly	aat Asn	tcc Ser	atc Ile	ttc Phe	cag Gln	atc Ile	aat Asn	atg Met	atc Ile	aag Lys	tac Tyr	atc Ile	aaa Lys	920

280								285				290				
gac	aaa	tac	cct	aat	ctc	caa	gtc	att	gga	ggc	aat	gtg	gtc	act	gct	968
Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	Val	Thr	Ala	
			295					300					305			
gcc	cag	gcc	aag	aac	ctc	att	gat	gca	ggc	gtg	gat	gcc	ctg	cgg	gtg	1016
Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala	Leu	Arg	Val	
		310					315					320				
ggc	atg	gga	agt	ggc	tcc	atc	tgc	att	acg	cag	gaa	gtg	ctg	gcc	tgt	1064
Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	Leu	Ala	Cys	
	325					330					335					
ggg	cgg	ccc	caa	gca	aca	gca	gtg	tac	aag	gtg	tca	gag	tat	gca	cgg	1112
Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu	Tyr	Ala	Arg	
	340				345					350					355	
cgc	ttt	ggc	gtt	ccg	gtc	att	gct	gat	gga	gga	atc	caa	aat	gtg	ggc	1160
Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln	Asn	Val	Gly	
				360					365					370		
cat	att	gcg	aaa	gcc	ttg	gcc	ctt	ggg	gcc	tcc	aca	gtc	atg	atg	ggc	1208
His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	Met	Met	Gly	
			375					380					385			
tct	ctc	ctg	gct	gcc	acc	act	gag	gcc	cct	ggc	gaa	tac	ttc	ttt	tcc	1256
Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	Phe	Phe	Ser	
		390					395					400				
gat	ggg	atc	cgg	cta	aag	aaa	tat	cgc	ggc	atg	ggc	tct	ctc	gat	gcc	1304
Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser	Leu	Asp	Ala	
	405					410					415					
atg	gac	aag	cac	ctc	agc	agc	cag	aac	aga	tat	ttc	agt	gaa	gct	gac	1352
Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser	Glu	Ala	Asp	
	420				425					430					435	
aaa	atc	aaa	gtg	gcc	cag	gga	gtg	tct	ggc	gct	gtg	cag	gac	aaa	ggg	1400
Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln	Asp	Lys	Gly	
				440					445					450		
tca	atc	cac	aaa	ttt	gtc	cct	tac	ctg	att	act	ggc	atc	caa	cac	tca	1448
Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Thr	Gly	Ile	Gln	His	Ser	
			455					460					465			
tgc	cag	gac	att	ggc	gcc	aag	agc	ttg	acc	caa	gtc	cga	gcc	atg	atg	1496
Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg	Ala	Met	Met	
		470					475					480				
tac	tct	ggg	gag	ctt	aag	ttt	gag	aag	aga	acg	tcc	tca	gcc	cag	gtg	1544
Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser	Ala	Gln	Val	
	485					490					495					
gaa	ggc	ggc	gtc	cat	agc	ctc	cat	tgc	tat	gag	aag	cgg	ctt	ttc		1589
Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg	Leu	Phe		
	500				505					510						
tgaaaaggga	tccagcacac	ctcctcggtt	tttttttcaa	taaaagttaa	gaaagaccg											1649
aattc																1654

<210> 10
 <211> 514
 <212> PRT
 <213> Homo sapien

<400> 10
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
 1 5 10 15
 Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
 20 25 30
 Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35 40 45
 Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50 55 60
 Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
 65 70 75 80
 Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95
 Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
 100 105 110
 Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
 115 120 125
 Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
 130 135 140
 Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
 145 150 155 160
 Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
 165 170 175
 Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Arg Ser Ile
 180 185 190
 Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
 195 200 205
 Leu Pro Ile Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg
 210 215 220
 Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
 225 230 235 240
 Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
 245 250 255
 Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val
 260 265 270
 Leu Asp Ser Ser Arg Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
 275 280 285
 Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
 290 295 300
 Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
 305 310 315 320
 Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val
 325 330 335
 Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
 340 345 350
 Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
 355 360 365
 Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
 370 375 380
 Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
 385 390 395 400
 Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
 405 410 415
 Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
 420 425 430
 Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
 435 440 445
 Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Thr Gly Ile
 450 455 460
 Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
 465 470 475 480
 Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
 485 490 495
 Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
 500 505 510

```
<221> CDS
<222> (48)...(1589)
<223> Phe456Ser/Asp470Gly Human IMPDH II mutant
```

aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cgg gat gtt ttt 440
Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp Val Phe
120 125 130

gag	gcc	aag	gcc	cgg	cat	ggt	ttc	tgc	ggt	atc	cca	atc	aca	gac	aca	488
Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile	Thr	Asp	Thr	
			135					140					145			
ggc	cgg	atg	ggg	agc	cgc	ttg	gtg	ggc	atc	atc	tcc	tcc	agg	gac	att	536
Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser	Arg	Asp	Ile	
		150					155					160				
gat	ttt	ctc	aaa	gag	gag	gaa	cat	gac	tgt	ttc	ttg	gaa	gag	ata	atg	584
Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Cys	Phe	Leu	Glu	Glu	Ile	Met	
	165					170					175					
aca	aag	agg	gaa	gac	ttg	gtg	gta	gcc	ccc	cgc	agc	atc	aca	ctg	aag	632
Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Arg	Ser	Ile	Thr	Leu	Lys	
180					185					190					195	
gag	gca	aat	gaa	att	ctg	cag	cgc	agc	aag	aag	gga	aag	ttg	ccc	att	680
Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys	Leu	Pro	Ile	
				200					205					210		
gta	aat	gaa	gat	gat	gag	ctt	gtg	gcc	atc	att	gcc	cgg	aca	gac	ctg	728
Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg	Thr	Asp	Leu	
			215					220					225			
aag	aag	aat	cgg	gac	tac	cca	cta	gcc	tcc	aaa	gat	gcc	aag	aaa	cag	776
Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala	Lys	Lys	Gln	
		230					235					240				
ctg	ctg	tgt	ggg	gca	gcc	att	ggc	act	cat	gag	gat	gac	aag	tat	agg	824
Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp	Lys	Tyr	Arg	
	245					250					255					
ctg	gac	ttg	ctc	gcc	cag	gct	ggt	gtg	gat	gta	gtg	gtt	ttg	gac	tct	872
Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val	Leu	Asp	Ser	
260					265				270						275	
tcc	cag	gga	aat	tcc	atc	ttc	cag	atc	aat	atg	atc	aag	tac	atc	aaa	920
Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys	Tyr	Ile	Lys	
				280					285					290		
gac	aaa	tac	cct	aat	ctc	caa	gtc	att	gga	ggc	aat	gtg	gtc	act	gct	968
Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	Val	Thr	Ala	
			295					300					305			
gcc	cag	gcc	aag	aac	ctc	att	gat	gca	ggt	gtg	gat	gcc	ctg	cgg	gtg	1016
Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala	Leu	Arg	Val	
		310					315					320				
ggc	atg	gga	agt	ggc	tcc	atc	tgc	att	acg	cag	gaa	gtg	ctg	gcc	tgt	1064
Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	Leu	Ala	Cys	
	325					330					335					
ggg	cgg	ccc	caa	gca	aca	gca	gtg	tac	aag	gtg	tca	gag	tat	gca	cgg	1112
Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu	Tyr	Ala	Arg	
340					345					350					355	
cgc	ttt	ggt	gtt	ccg	gtc	att	gct	gat	gga	gga	atc	caa	aat	gtg	ggt	1160
Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln	Asn	Val	Gly	
				360					365					370		
cat	att	gcg	aaa	gcc	ttg	gcc	ctt	ggg	gcc	tcc	aca	gtc	atg	atg	ggc	1208
His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	Met	Met	Gly	
			375					380					385			
tct	ctc	ctg	gct	gcc	acc	act	gag	gcc	cct	ggt	gaa	tac	ttc	ttt	tcc	1256

Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	Phe	Phe	Ser		
		390					395					400					
gat	ggg	atc	cgg	cta	aag	aaa	tat	cgc	ggg	atg	ggg	tct	ctc	gat	gcc		1304
Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser	Leu	Asp	Ala		
	405					410					415						
atg	gac	aag	cac	ctc	agc	agc	cag	aac	aga	tat	ttc	agt	gaa	gct	gac		1352
Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser	Glu	Ala	Asp		
	420				425					430					435		
aaa	atc	aaa	gtg	gcc	cag	gga	gtg	tct	ggg	gct	gtg	cag	gac	aaa	ggg		1400
Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln	Asp	Lys	Gly		
				440					445					450			
tca	atc	cac	aaa	tct	gtc	cct	tac	ctg	att	gct	ggc	atc	caa	cac	tca		1448
Ser	Ile	His	Lys	Ser	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile	Gln	His	Ser		
			455					460					465				
tgc	cag	ggc	att	ggg	gcc	aag	agc	ttg	acc	caa	gtc	cga	gcc	atg	atg		1496
Cys	Gln	Gly	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg	Ala	Met	Met		
		470					475					480					
tac	tct	ggg	gag	ctt	aag	ttt	gag	aag	aga	acg	tcc	tca	gcc	cag	gtg		1544
Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser	Ala	Gln	Val		
	485					490					495						
gaa	ggg	ggc	gtc	cat	agc	ctc	cat	tcg	tat	gag	aag	cgg	ctt	ttc			1589
Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg	Leu	Phe			
	500				505					510							
tgaaaaggga	tccagcacac	ctcctcggtt	tttttttcaa	taaaagttaa	gaaagacccg												1649
aattc																	1654

<210> 12
 <211> 514
 <212> PRT
 <213> Homo sapien

<400> 12

Met	Ala	Asp	Tyr	Leu	Ile	Ser	Gly	Gly	Thr	Ser	Tyr	Val	Pro	Asp	Asp		
1				5					10					15			
Gly	Leu	Thr	Ala	Gln	Gln	Leu	Phe	Asn	Cys	Gly	Asp	Gly	Leu	Thr	Tyr		
			20					25					30				
Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Tyr	Ile	Asp	Phe	Thr	Ala	Asp	Gln		
		35					40					45					
Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys	Thr	Pro		
	50					55					60						
Leu	Val	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	Ala	Ile		
	65				70					75					80		
Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr		
				85				90						95			
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln		
			100					105					110				
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg		
	115					120						125					
Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile		
	130				135						140						
Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser		
	145				150					155					160		
Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Cys	Phe	Leu	Glu		
				165				170						175			
Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Arg	Ser	Ile		
			180					185					190				
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys		

Leu	Pro	Ile	Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg
210						215					220				
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala
225					230					235					240
Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp
				245					250					255	
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val
			260					265					270		
Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys
	275					280						285			
Tyr	Ile	Lys	Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val
290						295					300				
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala
305				310						315					320
Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val
				325				330						335	
Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu
			340					345					350		
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln
		355					360				365				
Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val
370						375					380				
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr
385				390						395					400
Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser
			405					410					415		
Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser
			420					425				430			
Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln
		435					440					445			
Asp	Lys	Gly	Ser	Ile	His	Lys	Ser	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile
450						455					460				
Gln	His	Ser	Cys	Gln	Gly	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg
465				470						475					480
Ala	Met	Met	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser
				485					490					495	
Ala	Gln	Val	Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg
		500						505					510		

Leu Phe

<210> 13
 <211> 1994
 <212> DNA
 <213> Tritrichomonas foetus

<220>
 <221> CDS
 <222> (115)...(1623)
 <223> T. foetus IMPDH Type II

<300>
 <301> Beck, J.T., Zhao, S. and Wang, C.C.
 <302> Cloning, sequencing, and structural analysis of th
 <303> Exp. Parasitol. (1994)
 <304> 78
 <305> 1
 <306> 101-112

<400> 13
 tcatatagca aaaagccata aacaattcaa aacatgtatt gaattcgtgc atgaccatcc 60
 ttcacatttc atctcacata gcttttttat ttttttcatt gtaagtccaa acaa atg 117
 Met
 1

gca	aaa	tac	tac	aac	gaa	cca	tgc	cac	acc	ttt	aac	gaa	tat	ctc	ctc	165
Ala	Lys	Tyr	Tyr	Asn	Glu	Pro	Cys	His	Thr	Phe	Asn	Glu	Tyr	Leu	Leu	
		5					10						15			
att	cca	gga	ctc	tca	aca	gtc	gac	tgc	att	cca	tcc	aac	gtt	aac	tta	213
Ile	Pro	Gly	Leu	Ser	Thr	Val	Asp	Cys	Ile	Pro	Ser	Asn	Val	Asn	Leu	
		20					25					30				
tct	acc	cca	ctc	gtc	aag	ttc	caa	aag	ggg	caa	caa	agt	gag	atc	aat	261
Ser	Thr	Pro	Leu	Val	Lys	Phe	Gln	Lys	Gly	Gln	Gln	Ser	Glu	Ile	Asn	
	35					40					45					
tta	aag	atc	ccc	ctt	gtt	tct	gcc	atc	atg	caa	tct	gtc	tca	gga	gaa	309
Leu	Lys	Ile	Pro	Leu	Val	Ser	Ala	Ile	Met	Gln	Ser	Val	Ser	Gly	Glu	
	50				55					60					65	
aag	atg	gct	atc	gca	ttg	gca	cga	gaa	ggg	ggg	att	tca	ttc	att	ttc	357
Lys	Met	Ala	Ile	Ala	Leu	Ala	Arg	Glu	Gly	Gly	Ile	Ser	Phe	Ile	Phe	
				70					75					80		
gga	tct	caa	tca	att	gaa	agc	caa	gca	gcc	atg	gtc	cat	gct	gtc	aaa	405
Gly	Ser	Gln	Ser	Ile	Glu	Ser	Gln	Ala	Ala	Met	Val	His	Ala	Val	Lys	
			85					90					95			
aat	ttc	aaa	gcc	ggc	ttt	gtc	gtc	tca	gat	tca	aac	gtt	aaa	cca	gat	453
Asn	Phe	Lys	Ala	Gly	Phe	Val	Val	Ser	Asp	Ser	Asn	Val	Lys	Pro	Asp	
		100					105					110				
caa	aca	ttt	gct	gat	gtt	tta	gca	att	tct	caa	cga	aca	acc	cac	aac	501
Gln	Thr	Phe	Ala	Asp	Val	Leu	Ala	Ile	Ser	Gln	Arg	Thr	Thr	His	Asn	
	115					120					125					
act	gtc	gct	gtc	aca	gac	gat	gga	act	cca	cat	gga	gtt	tta	ctt	ggg	549
Thr	Val	Ala	Val	Thr	Asp	Asp	Gly	Thr	Pro	His	Gly	Val	Leu	Leu	Gly	
	130				135					140					145	
ttg	gtc	act	caa	cgc	gat	tat	cca	atc	gat	ctt	acc	cag	acc	gaa	aca	597
Leu	Val	Thr	Gln	Arg	Asp	Tyr	Pro	Ile	Asp	Leu	Thr	Gln	Thr	Glu	Thr	
				150					155					160		
aag	gtt	tcc	gac	atg	atg	aca	cca	ttc	agc	aag	ctc	gtt	aca	gcc	cat	645
Lys	Val	Ser	Asp	Met	Met	Thr	Pro	Phe	Ser	Lys	Leu	Val	Thr	Ala	His	
			165					170					175			
cag	gac	aca	aaa	ctt	tca	gaa	gcc	aac	aaa	att	att	tgg	gag	aag	aaa	693
Gln	Asp	Thr	Lys	Leu	Ser	Glu	Ala	Asn	Lys	Ile	Ile	Trp	Glu	Lys	Lys	
		180					185					190				
tta	aat	gct	ctt	cct	atc	att	gat	gac	gat	caa	cat	ctt	cgt	tat	atc	741
Leu	Asn	Ala	Leu	Pro	Ile	Ile	Asp	Asp	Asp	Gln	His	Leu	Arg	Tyr	Ile	
	195					200					205					
gtt	ttc	cgc	aaa	gat	tat	gac	aga	tcg	caa	gtc	tgt	cac	aac	gaa	ctc	789
Val	Phe	Arg	Lys	Asp	Tyr	Asp	Arg	Ser	Gln	Val	Cys	His	Asn	Glu	Leu	
	210				215					220					225	
gtc	gat	tcg	caa	aaa	cgc	tat	ttg	gtc	gga	gca	gga	att	aac	aca	cgc	837
Val	Asp	Ser	Gln	Lys	Arg	Tyr	Leu	Val	Gly	Ala	Gly	Ile	Asn	Thr	Arg	
				230					235					240		
gac	ttc	aga	gaa	cgc	gtt	cca	gca	ctt	gtc	gaa	gcc	ggc	gct	gat	gtc	885
Asp	Phe	Arg	Glu	Arg	Val	Pro	Ala	Leu	Val	Glu	Ala	Gly	Ala	Asp	Val	
			245					250					255			

ctt tgc att gat tcc agc gac ggc ttc tca gaa tgg cag aaa att aca	933
Leu Cys Ile Asp Ser Ser Asp Gly Phe Ser Glu Trp Gln Lys Ile Thr	
260 265 270	
atc ggc tgg att cgc gag aaa tac ggc gat aaa gtt aaa gtt ggt gcg	981
Ile Gly Trp Ile Arg Glu Lys Tyr Gly Asp Lys Val Lys Val Gly Ala	
275 280 285	
gga aac att gtt gac ggt gaa gga ttc cgc tat ttg gcc gac gct gga	1029
Gly Asn Ile Val Asp Gly Glu Gly Phe Arg Tyr Leu Ala Asp Ala Gly	
290 295 300 305	
gct gat ttc atc aag att gga att ggc ggt gga tca att tgc atc aca	1077
Ala Asp Phe Ile Lys Ile Gly Ile Gly Gly Gly Ser Ile Cys Ile Thr	
310 315 320	
cgc gag cag aaa ggt atc ggc cga ggc caa gct act gcc gtc att gat	1125
Arg Glu Gln Lys Gly Ile Gly Arg Gly Gln Ala Thr Ala Val Ile Asp	
325 330 335	
ggt gtt gca gag cgt aac aaa tac ttc gaa gag acc gga att tat atc	1173
Val Val Ala Glu Arg Asn Lys Tyr Phe Glu Glu Thr Gly Ile Tyr Ile	
340 345 350	
cct gtt tgc tct gat ggt gga att gtt tat gat tat cac atg aca ctt	1221
Pro Val Cys Ser Asp Gly Gly Ile Val Tyr Asp Tyr His Met Thr Leu	
355 360 365	
gct ctt gca atg ggc gca gat ttc atc atg ctt ggc agg tac ttc gcc	1269
Ala Leu Ala Met Gly Ala Asp Phe Ile Met Leu Gly Arg Tyr Phe Ala	
370 375 380 385	
cgt ttt gag gag tca cca aca aga aaa gtg aca att aat gga agc gtt	1317
Arg Phe Glu Glu Ser Pro Thr Arg Lys Val Thr Ile Asn Gly Ser Val	
390 395 400	
atg aag gag tac tgg gga gaa ggc tct tcg cgc gct agg aac tgg cag	1365
Met Lys Glu Tyr Trp Gly Glu Gly Ser Ser Arg Ala Arg Asn Trp Gln	
405 410 415	
cgc tat gac ctt gga ggt aag cag aag ctt tcc ttt gaa gag gga gtc	1413
Arg Tyr Asp Leu Gly Gly Lys Gln Lys Leu Ser Phe Glu Glu Gly Val	
420 425 430	
gat tct tac gtc cca tac gct gga aag ttg aag gac aac gtg gag gca	1461
Asp Ser Tyr Val Pro Tyr Ala Gly Lys Leu Lys Asp Asn Val Glu Ala	
435 440 445	
tcc ttg aac aag gta aaa tca acg atg tgc aac tgt gga gcg ctc aca	1509
Ser Leu Asn Lys Val Lys Ser Thr Met Cys Asn Cys Gly Ala Leu Thr	
450 455 460 465	
atc ccg cag ctc cag agc aag gca aag atc aca ctt gta tca tca gtt	1557
Ile Pro Gln Leu Gln Ser Lys Ala Lys Ile Thr Leu Val Ser Ser Val	
470 475 480	
tca att gtc gaa gga ggc gca cac gat gtt att gtt aag gac agg att	1605
Ser Ile Val Glu Gly Gly Ala His Asp Val Ile Val Lys Asp Arg Ile	
485 490 495	
aac gac tat cac cca aaa taaatatatt gttttataact ttatgtttgt	1653
Asn Asp Tyr His Pro Lys	
500	
taaattatac ctatttactt ctcttgtttt tatgtctttt gattcttcca tgtctttgaa	1713


```

ttcttccatg tcttttgatt ctttttccca catggtgcat gtggtgaatt attcaaaacc 1773
cttttccttt gtaacttgtc attaattggc attttcggag tgaactagtt aattattttt 1833
ccaatgatat ttattatagt ctttttgtgt attgatgtct tactttactg atagtgatta 1893
gggtcaatact ctattatgga gtctgactcg cggtactcta tctatattaa ctataacaca 1953
tagcttagtc tacactgcgt agctcttggt acttgacatg a 1994

```

<210> 14
 <211> 503
 <212> PRT
 <213> Tritrichomonas foetus

<400> 14

Met	Ala	Lys	Tyr	Tyr	Asn	Glu	Pro	Cys	His	Thr	Phe	Asn	Glu	Tyr	Leu	
1				5					10					15		
Leu	Ile	Pro	Gly	Leu	Ser	Thr	Val	Asp	Cys	Ile	Pro	Ser	Asn	Val	Asn	
			20					25					30			
Leu	Ser	Thr	Pro	Leu	Val	Lys	Phe	Gln	Lys	Gly	Gln	Gln	Ser	Glu	Ile	
		35					40					45				
Asn	Leu	Lys	Ile	Pro	Leu	Val	Ser	Ala	Ile	Met	Gln	Ser	Val	Ser	Gly	
	50					55					60					

Glu	Lys	Met	Ala	Ile	Ala	Leu	Ala	Arg	Glu	Gly	Gly	Ile	Ser	Phe	Ile	
65					70					75					80	
Phe	Gly	Ser	Gln	Ser	Ile	Glu	Ser	Gln	Ala	Ala	Met	Val	His	Ala	Val	
			85					90						95		
Lys	Asn	Phe	Lys	Ala	Gly	Phe	Val	Val	Ser	Asp	Ser	Asn	Val	Lys	Pro	
		100						105					110			
Asp	Gln	Thr	Phe	Ala	Asp	Val	Leu	Ala	Ile	Ser	Gln	Arg	Thr	Thr	His	
		115					120					125				
Asn	Thr	Val	Ala	Val	Thr	Asp	Asp	Gly	Thr	Pro	His	Gly	Val	Leu	Leu	
	130					135						140				
Gly	Leu	Val	Thr	Gln	Arg	Asp	Tyr	Pro	Ile	Asp	Leu	Thr	Gln	Thr	Glu	
145				150						155					160	
Thr	Lys	Val	Ser	Asp	Met	Met	Thr	Pro	Phe	Ser	Lys	Leu	Val	Thr	Ala	
			165						170					175		
His	Gln	Asp	Thr	Lys	Leu	Ser	Glu	Ala	Asn	Lys	Ile	Ile	Trp	Glu	Lys	
		180						185					190			
Lys	Leu	Asn	Ala	Leu	Pro	Ile	Ile	Asp	Asp	Asp	Gln	His	Leu	Arg	Tyr	
	195						200					205				
Ile	Val	Phe	Arg	Lys	Asp	Tyr	Asp	Arg	Ser	Gln	Val	Cys	His	Asn	Glu	
	210				215						220					
Leu	Val	Asp	Ser	Gln	Lys	Arg	Tyr	Leu	Val	Gly	Ala	Gly	Ile	Asn	Thr	
225				230						235					240	
Arg	Asp	Phe	Arg	Glu	Arg	Val	Pro	Ala	Leu	Val	Glu	Ala	Gly	Ala	Asp	
			245						250					255		
Val	Leu	Cys	Ile	Asp	Ser	Ser	Asp	Gly	Phe	Ser	Glu	Trp	Gln	Lys	Ile	
		260						265					270			
Thr	Ile	Gly	Trp	Ile	Arg	Glu	Lys	Tyr	Gly	Asp	Lys	Val	Lys	Val	Gly	
	275						280					285				
Ala	Gly	Asn	Ile	Val	Asp	Gly	Glu	Gly	Phe	Arg	Tyr	Leu	Ala	Asp	Ala	
	290					295					300					
Gly	Ala	Asp	Phe	Ile	Lys	Ile	Gly	Ile	Gly	Gly	Gly	Ser	Ile	Cys	Ile	
305				310						315					320	
Thr	Arg	Glu	Gln	Lys	Gly	Ile	Gly	Arg	Gly	Gln	Ala	Thr	Ala	Val	Ile	
			325						330					335		
Asp	Val	Val	Ala	Glu	Arg	Asn	Lys	Tyr	Phe	Glu	Glu	Thr	Gly	Ile	Tyr	
		340						345					350			
Ile	Pro	Val	Cys	Ser	Asp	Gly	Gly	Ile	Val	Tyr	Asp	Tyr	His	Met	Thr	
	355					360					365					
Leu	Ala	Leu	Ala	Met	Gly	Ala	Asp	Phe	Ile	Met	Leu	Gly	Arg	Tyr	Phe	
	370				375						380					
Ala	Arg	Phe	Glu	Glu	Ser	Pro	Thr	Arg	Lys	Val	Thr	Ile	Asn	Gly	Ser	
385				390						395					400	
Val	Met	Lys	Glu	Tyr	Trp	Gly	Glu	Gly	Ser	Ser	Arg	Ala	Arg	Asn	Trp	
			405					410						415		
Gln	Arg	Tyr	Asp	Leu	Gly	Gly	Lys	Gln	Lys	Leu	Ser	Phe	Glu	Glu	Gly	

Val	Asp	Ser	Tyr	Val	Pro	Tyr	Ala	Gly	Lys	Leu	Lys	Asp	Asn	Val	Glu
		435					440					445			
Ala	Ser	Leu	Asn	Lys	Val	Lys	Ser	Thr	Met	Cys	Asn	Cys	Gly	Ala	Leu
	450					455					460				
Thr	Ile	Pro	Gln	Leu	Gln	Ser	Lys	Ala	Lys	Ile	Thr	Leu	Val	Ser	Ser
465					470					475					480
Val	Ser	Ile	Val	Glu	Gly	Gly	Ala	His	Asp	Val	Ile	Val	Lys	Asp	Arg
			485					490						495	
Ile	Asn	Asp	Tyr	His	Pro	Lys									
			500												

<210> 15

<211> 1560

<212> DNA

<213> Aspergillus nidulans

<220>

<221> CDS

<222> (1)...(1560)

<223> Aspergillus nidulans wild type DHODH cDNA

<400> 15

atg	gct	acg	aat	tct	ttc	cga	aaa	ctc	act	ttt	tca	gga	gcc	tcc	cgt	48
Met	Ala	Thr	Asn	Ser	Phe	Arg	Lys	Leu	Thr	Phe	Ser	Gly	Ala	Ser	Arg	
1				5					10					15		

ctg	ggt	ggt	tgt	cgc	cgt	ctc	cca	cta	acc	tgc	aga	caa	ctt	cga	ttc	96
Leu	Gly	Gly	Cys	Arg	Arg	Leu	Pro	Leu	Thr	Cys	Arg	Gln	Leu	Arg	Phe	
			20					25					30			

gcc	tcc	gac	agc	gga	gcc	gca	gcg	gca	act	aca	aaa	gca	acg	gcc	gaa	144
Ala	Ser	Asp	Ser	Gly	Ala	Ala	Ala	Ala	Thr	Thr	Lys	Ala	Thr	Ala	Glu	
		35				40						45				

tca	gca	gcc	gag	tca	gct	agt	ata	aac	gtc	aaa	gag	gca	ccc	aaa	aag	192
Ser	Ala	Ala	Glu	Ser	Ala	Ser	Ile	Asn	Val	Lys	Glu	Ala	Pro	Lys	Lys	
	50					55					60					

gcc	gga	cgg	ggc	ctg	cgg	cgc	acg	gtc	ctg	gga	acg	tcg	ttg	gcg	ctg	240
Ala	Gly	Arg	Gly	Leu	Arg	Arg	Thr	Val	Leu	Gly	Thr	Ser	Leu	Ala	Leu	
65					70					75					80	

acg	ctg	ctg	gtt	gga	tat	gtc	tac	ggg	acg	gac	acc	cgg	gcg	agt	gtg	288
Thr	Leu	Leu	Val	Gly	Tyr	Val	Tyr	Gly	Thr	Asp	Thr	Arg	Ala	Ser	Val	
			85					90						95		

cat	cgg	tac	ggt	gtt	gtg	ccg	ctg	att	aga	gca	ttg	tat	cct	gat	gcg	336
His	Arg	Tyr	Gly	Val	Val	Pro	Leu	Ile	Arg	Ala	Leu	Tyr	Pro	Asp	Ala	
			100					105					110			

gaa	gat	gcg	cat	cat	att	ggt	gtc	gat	act	tta	aag	atg	ctg	tat	aag	384
Glu	Asp	Ala	His	His	Ile	Gly	Val	Asp	Thr	Leu	Lys	Met	Leu	Tyr	Lys	
		115					120					125				

tat	ggt	ctg	cat	cca	agg	gaa	cgg	ggg	gat	ccg	gat	gga	gat	ggg	gcg	432
Tyr	Gly	Leu	His	Pro	Arg	Glu	Arg	Gly	Asp	Pro	Asp	Gly	Asp	Gly	Ala	
	130					135					140					

ctg	gcg	aca	gag	gtc	ttt	ggg	tat	aca	ctg	tca	aac	cca	att	ggc	ata	480
Leu	Ala	Thr	Glu	Val	Phe	Gly	Tyr	Thr	Leu	Ser	Asn	Pro	Ile	Gly	Ile	
145					150					155					160	

tcg	ggc	ggc	ctg	gac	aag	cat	gct	gag	atc	cct	gat	ccg	ctg	ttc	gcg	528
Ser	Gly	Gly	Leu	Asp	Lys	His	Ala	Glu	Ile	Pro	Asp	Pro	Leu	Phe	Ala	

165				170				175								
atc	ggt	cct	gcc	att	gtc	gaa	gtc	ggg	ggt	acg	aca	ccc	tta	cca	cag	576
Ile	Gly	Pro	Ala	Ile	Val	Glu	Val	Gly	Gly	Thr	Thr	Pro	Leu	Pro	Gln	
			180					185					190			
gat	ggt	aac	ccg	cgt	cct	cgc	gta	ttc	cga	ctt	cca	tca	cag	aga	gcg	624
Asp	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Ser	Gln	Arg	Ala	
		195					200					205				
atg	ata	aac	cgg	tac	ggc	ctc	aac	tcc	aaa	ggc	gca	gat	cac	atg	gca	672
Met	Ile	Asn	Arg	Tyr	Gly	Leu	Asn	Ser	Lys	Gly	Ala	Asp	His	Met	Ala	
	210					215					220					
gct	atc	ttg	gag	caa	cga	gta	cgc	gat	ttt	gcc	tac	gca	aac	gga	ttt	720
Ala	Ile	Leu	Glu	Gln	Arg	Val	Arg	Asp	Phe	Ala	Tyr	Ala	Asn	Gly	Phe	
225					230					235					240	
ggg	gca	tac	gat	gcg	gct	aag	cag	cgt	gta	ttg	gac	ggc	gaa	gct	ggt	768
Gly	Ala	Tyr	Asp	Ala	Ala	Lys	Gln	Arg	Val	Leu	Asp	Gly	Glu	Ala	Gly	
				245					250				255			
gtg	cca	cca	ggt	agt	ctt	cag	cct	ggt	aag	ctt	tta	gct	gtc	caa	gtg	816
Val	Pro	Pro	Gly	Ser	Leu	Gln	Pro	Gly	Lys	Leu	Leu	Ala	Val	Gln	Val	
			260					265					270			
gca	aag	aac	aag	gcc	act	cct	gac	ggc	gac	att	gaa	gcc	atc	aag	cgc	864
Ala	Lys	Asn	Lys	Ala	Thr	Pro	Asp	Gly	Asp	Ile	Glu	Ala	Ile	Lys	Arg	
		275					280					285				
gac	tat	gtg	tat	tgc	gtg	gac	cgt	gtg	gcc	aaa	tac	gct	gat	att	ctt	912
Asp	Tyr	Val	Tyr	Cys	Val	Asp	Arg	Val	Ala	Lys	Tyr	Ala	Asp	Ile	Leu	
	290					295					300					
gtt	gtg	aat	gta	tcg	agc	ccc	aac	aca	ccc	ggt	ctc	cgt	gac	ctt	caa	960
Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly	Leu	Arg	Asp	Leu	Gln	
305					310					315					320	
gcc	act	gcc	ccg	ctc	aca	gct	atc	ttg	agt	gct	gtc	gtt	ggc	gcg	gca	1008
Ala	Thr	Ala	Pro	Leu	Thr	Ala	Ile	Leu	Ser	Ala	Val	Val	Gly	Ala	Ala	
				325				330					335			
aag	agc	gtg	aac	cgc	aag	acc	aaa	cca	tat	gtt	atg	gtc	aag	gtc	agt	1056
Lys	Ser	Val	Asn	Arg	Lys	Thr	Lys	Pro	Tyr	Val	Met	Val	Lys	Val	Ser	
			340					345					350			
ccg	gat	gaa	gac	tca	gat	gaa	caa	gtc	tct	ggt	atc	tgc	gac	gcc	gtc	1104
Pro	Asp	Glu	Asp	Ser	Asp	Glu	Gln	Val	Ser	Gly	Ile	Cys	Asp	Ala	Val	
		355					360					365				
cga	gca	tcc	ggt	gtc	gac	gga	gtg	att	gtc	gga	aac	aca	aca	aac	cgt	1152
Arg	Ala	Ser	Gly	Val	Asp	Gly	Val	Ile	Val	Gly	Asn	Thr	Thr	Asn	Arg	
	370					375					380					
cgc	ccc	gac	cct	ata	ccc	caa	ggt	tac	act	ctt	ccg	gcc	aag	gag	cag	1200
Arg	Pro	Asp	Pro	Ile	Pro	Gln	Gly	Tyr	Thr	Leu	Pro	Ala	Lys	Glu	Gln	
385					390					395					400	
gca	acg	ttg	aaa	gaa	acc	ggc	ggg	tat	tca	ggt	cca	cag	ctg	ttc	gat	1248
Ala	Thr	Leu	Lys	Glu	Thr	Gly	Gly	Tyr	Ser	Gly	Pro	Gln	Leu	Phe	Asp	
				405				410						415		
cgc	aca	gtg	gcc	ctt	gtg	gct	cgg	tac	cgc	tcc	atg	ctg	gat	gcg	gag	1296
Arg	Thr	Val	Ala	Leu	Val	Ala	Arg	Tyr	Arg	Ser	Met	Leu	Asp	Ala	Glu	
			420					425					430			

tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa	1344
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln	
435 440 445	
aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga	1392
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly	
450 455 460	
ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag	1440
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys	
465 470 475 480	
cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac	1488
Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr	
485 490 495	
acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa	1536
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln	
500 505 510	
gaa ctt cga acg gcg aaa aag gag	1560
Glu Leu Arg Thr Ala Lys Lys Glu	
515 520	

<210> 16
 <211> 520
 <212> PRT
 <213> Aspergillus nidulans

<400> 16

Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg	
1 5 10 15	
Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe	
20 25 30	
Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu	
35 40 45	
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys	
50 55 60	
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu	
65 70 75 80	
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val	
85 90 95	
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala	
100 105 110	
Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys	
115 120 125	
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala	
130 135 140	
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile	
145 150 155 160	
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala	
165 170 175	
Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln	
180 185 190	
Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala	
195 200 205	
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala	
210 215 220	
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe	
225 230 235 240	
Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly	
245 250 255	
Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val	

Ala	Lys	Asn	Lys	Ala	Thr	Pro	Asp	Gly	Asp	Ile	Glu	Ala	Ile	Lys	Arg
		275					280					285			
Asp	Tyr	Val	Tyr	Cys	Val	Asp	Arg	Val	Ala	Lys	Tyr	Ala	Asp	Ile	Leu
	290					295					300				
Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly	Leu	Arg	Asp	Leu	Gln
305					310					315					320
Ala	Thr	Ala	Pro	Leu	Thr	Ala	Ile	Leu	Ser	Ala	Val	Val	Gly	Ala	Ala
			325						330					335	
Lys	Ser	Val	Asn	Arg	Lys	Thr	Lys	Pro	Tyr	Val	Met	Val	Lys	Val	Ser
		340						345					350		
Pro	Asp	Glu	Asp	Ser	Asp	Glu	Gln	Val	Ser	Gly	Ile	Cys	Asp	Ala	Val
	355					360						365			
Arg	Ala	Ser	Gly	Val	Asp	Gly	Val	Ile	Val	Gly	Asn	Thr	Thr	Asn	Arg
	370				375						380				
Arg	Pro	Asp	Pro	Ile	Pro	Gln	Gly	Tyr	Thr	Leu	Pro	Ala	Lys	Glu	Gln
385					390					395					400
Ala	Thr	Leu	Lys	Glu	Thr	Gly	Gly	Tyr	Ser	Gly	Pro	Gln	Leu	Phe	Asp
			405					410						415	
Arg	Thr	Val	Ala	Leu	Val	Ala	Arg	Tyr	Arg	Ser	Met	Leu	Asp	Ala	Glu
		420						425				430			
Ser	Glu	Thr	Ala	Gly	Ser	Ala	Lys	Asp	Ser	Ala	Ala	Thr	Ile	Ala	Gln
		435					440					445			
Thr	Glu	Pro	Gly	Ser	Glu	Asn	Val	Pro	Pro	Val	Glu	Ala	Pro	Ser	Gly
	450					455					460				
Leu	Pro	Arg	Lys	Val	Ile	Phe	Ala	Ser	Gly	Gly	Ile	Thr	Asn	Gly	Lys
465					470					475					480
Gln	Ala	His	Ala	Val	Leu	Asp	Thr	Gly	Ala	Ser	Val	Ala	Met	Met	Tyr
			485					490					495		
Thr	Gly	Val	Val	Tyr	Gly	Gly	Val	Gly	Thr	Val	Thr	Arg	Val	Lys	Gln
		500						505					510		
Glu	Leu	Arg	Thr	Ala	Lys	Lys	Glu								
	515						520								

<210> 17
 <211> 2858
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (601)...(2142)
 <223> Human wild-type IMPDH type I

<300>
 <301> Natsumeda et al.
 <302> Two Distinct cDNAs for Human IMP Dehydrogenase
 <303> J. Biol. Chem. (1990)
 <304> 265
 <305> 9
 <306> 5292-5295

<400> 17																
tcggaagggg	ccaggagaca	ctggaaggtc	cggacggcag	ggaaggggac	ggggttcttt											60
ccagtcccac	ccgtgtaggg	acacctctcc	ccctcatccc	ccgatgtacc	ctcgctgaat											120
ctgggatggg	agagacgaac	cgagtctagg	catctgcgta	gcagcgccgg	ggagagcggg											180
gagcccaggc	ggagcccagt	cgactcccgg	attcccctgc	cccgcctccg	gcacgaggcc											240
ccgccccggc	gccccgcccc	tcctcgggac	tcgaccgggc	tgcgctcact	gcccagccgg											300
ggccccggga	gcctccaggc	tcgccccgcc	tgagctgcgg	cctccgcatg	gagggccact											360
cactccacca	ccgctgcagg	gagggcgga	gcgctgttcc	ggagcccggg	gcccggcaac											420
acccgggaca	cgagacggcg	gcgcagggct	acagcgcccc	actgctgcag	gccggctacg											480
agcccagag	ccctagattg	gacctcgcta	cacacccgac	gacaccccgt	tcagaactat											540
cttcagtgg	cttactggca	ggtgttggtg	tccagatgga	tcgccttcgc	agggctagcc											600
atg gcg gac tac ctg atc agc ggc ggc acc ggc tac gtg ccc gag gat																648
Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Gly Tyr Val Pro Glu Asp																

1				5					10					15			
ggg	ctc	acc	gcg	cag	cag	ctc	ttc	gcc	agc	gcc	gac	gac	ctc	acc	tac		696
Gly	Leu	Thr	Ala	Gln	Gln	Leu	Phe	Ala	Ser	Ala	Asp	Asp	Leu	Thr	Tyr		
			20					25					30				
aac	gac	ttc	ctg	att	ctc	cca	gga	ttc	ata	gac	ttc	ata	gct	gat	gag		744
Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Phe	Ile	Asp	Phe	Ile	Ala	Asp	Glu		
		35					40					45					
gtg	gac	ctg	acc	tca	gcc	ctg	acc	cgg	aag	atc	acg	ctg	aag	acg	cca		792
Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Arg	Lys	Ile	Thr	Leu	Lys	Thr	Pro		
	50					55					60						
ctc	atc	tcc	tcc	ccc	atg	gac	act	gtg	aca	gag	gct	gac	atg	gcc	att		840
Leu	Ile	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Asp	Met	Ala	Ile		
65					70					75					80		
gcc	atg	gct	ctg	atg	gga	ggt	att	ggg	ttc	att	cac	cac	aac	tgc	acc		888
Ala	Met	Ala	Leu	Met	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr		
				85				90						95			
cca	gag	ttc	cag	gcc	aat	gaa	gta	cgc	aag	gtc	aag	aac	ttt	gaa	cag		936
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Asn	Phe	Glu	Gln		
			100					105					110				
ggc	ttc	atc	acg	gac	cct	gtg	gtg	ctg	agc	ccc	tcg	cac	act	gtg	ggc		984
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Ser	His	Thr	Val	Gly		
		115					120					125					
gat	gtg	ctg	gag	gcc	aag	atg	cgg	cat	ggc	ttc	tct	ggc	atc	ccc	atc		1032
Asp	Val	Leu	Glu	Ala	Lys	Met	Arg	His	Gly	Phe	Ser	Gly	Ile	Pro	Ile		
	130					135					140						
act	gag	acg	ggc	acc	atg	ggc	agc	aag	ctg	gtg	ggc	atc	gtc	acc	tcc		1080
Thr	Glu	Thr	Gly	Thr	Met	Gly	Ser	Lys	Leu	Val	Gly	Ile	Val	Thr	Ser		
145					150					155					160		
cga	gac	atc	gac	ttt	ctt	gct	gag	aag	gac	cac	acc	acc	ctc	ctc	agt		1128
Arg	Asp	Ile	Asp	Phe	Leu	Ala	Glu	Lys	Asp	His	Thr	Thr	Leu	Leu	Ser		
				165				170					175				
gag	gtg	atg	acg	cca	agg	att	gaa	ctg	gtg	gtg	gct	cca	gca	ggt	gtg		1176
Glu	Val	Met	Thr	Pro	Arg	Ile	Glu	Leu	Val	Val	Ala	Pro	Ala	Gly	Val		
			180					185					190				
acg	ttg	aaa	gag	gca	aat	gag	atc	ctg	cag	cgt	agc	aag	aaa	ggg	aag		1224
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys		
		195					200					205					
ctg	cct	atc	gtc	aat	gat	tgc	gat	gag	ctg	gtg	gcc	atc	atc	gcc	cgc		1272
Leu	Pro	Ile	Val	Asn	Asp	Cys	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg		
	210					215					220						
acc	gac	ctg	aag	aag	aat	cga	gac	tac	cct	ctg	gcc	tcc	aag	gat	tcc		1320
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ser		
225					230					235					240		
cag	aag	cag	ctg	ctc	tgt	ggg	gca	gct	gtg	ggc	acc	cgt	gag	gat	gac		1368
Gln	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Val	Gly	Thr	Arg	Glu	Asp	Asp		
				245					250					255			
aaa	tac	cgt	ctg	gac	ctg	ctg	acc	cag	gcg	ggg	gtc	gac	gtc	ata	gtc		1416
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Thr	Gln	Ala	Gly	Val	Asp	Val	Ile	Val		
			260					265					270				

ttc	cac	tcg	tcc	caa	ggg	aat	tcg	gtg	tat	cag	atc	gcc	atg	gtg	cat	1464
Phe	His	Ser	Ser	Gln	Gly	Asn	Ser	Val	Tyr	Gln	Ile	Ala	Met	Val	His	
		275					280					285				
tac	atc	aaa	cag	aag	tac	ccc	cac	ctc	cag	gtg	att	ggg	ggg	aac	gtg	1512
Tyr	Ile	Lys	Gln	Lys	Tyr	Pro	His	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	
	290					295					300					
gtg	aca	gca	gcc	cag	gcc	aag	aac	ctg	att	gat	gct	ggg	gtg	gac	ggg	1560
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Gly	
305					310					315					320	
ctg	cgc	gtg	ggc	atg	ggc	tgc	ggc	tcc	atc	tgc	atc	acc	cag	gaa	gtg	1608
Leu	Arg	Val	Gly	Met	Gly	Cys	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	
				325					330					335		
atg	gcc	tgt	ggg	cgg	ccc	cag	ggc	act	gct	gtg	tac	aag	gtg	gct	gag	1656
Met	Ala	Cys	Gly	Arg	Pro	Gln	Gly	Thr	Ala	Val	Tyr	Lys	Val	Ala	Glu	
			340					345					350			
tat	gcc	cgg	cgc	ttt	ggg	gtg	ccc	atc	ata	gcc	gat	ggc	ggc	atc	cag	1704
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Ile	Ile	Ala	Asp	Gly	Gly	Ile	Gln	
		355					360					365				
acc	gtg	gga	cac	gtg	gtc	aag	gcc	ctg	gcc	ctt	gga	gcc	tcc	aca	gtg	1752
Thr	Val	Gly	His	Val	Val	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	
	370					375					380					
atg	atg	ggc	tcc	ctg	ctg	gcc	gcc	act	acg	gag	gcc	cct	ggc	gag	tac	1800
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	
385					390					395					400	
ttc	ttc	tca	gac	ggg	gtg	cgg	ctc	aag	aag	tac	cgg	ggc	atg	ggc	tca	1848
Phe	Phe	Ser	Asp	Gly	Val	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser	
				405					410					415		
ctg	gat	ccc	atg	gag	aag	agc	agc	agc	agc	cag	aaa	cga	tac	ttc	agc	1896
Leu	Asp	Pro	Met	Glu	Lys	Ser	Ser	Ser	Ser	Gln	Lys	Arg	Tyr	Phe	Ser	
			420					425					430			
gag	ggg	gat	aaa	gtg	aag	atc	gca	cag	ggg	gtc	tcg	ggc	tcc	atc	cag	1944
Glu	Gly	Asp	Lys	Val	Lys	Ile	Ala	Gln	Gly	Val	Ser	Gly	Ser	Ile	Gln	
		435					440					445				
gac	aaa	gga	tcc	att	cag	aag	ttc	gtg	ccc	tac	ctc	ata	gca	ggc	atc	1992
Asp	Lys	Gly	Ser	Ile	Gln	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile	
	450					455					460					
caa	cac	ggc	tgc	cag	gat	atc	ggg	gcc	cgc	agc	ctg	tct	gtc	ctt	cgg	2040
Gln	His	Gly	Cys	Gln	Asp	Ile	Gly	Ala	Arg	Ser	Leu	Ser	Val	Leu	Arg	
465					470					475					480	
tcc	atg	atg	tac	tca	gga	gag	ctc	aag	ttt	gag	aag	cgg	acc	atg	tcg	2088
Ser	Met	Met	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Met	Ser	
				485					490					495		
ccc	cag	att	gag	ggg	ggg	gtc	cat	ggc	ctg	cac	tct	tac	gaa	aag	cgg	2136
Pro	Gln	Ile	Glu	Gly	Gly	Val	His	Gly	Leu	His	Ser	Tyr	Glu	Lys	Arg	
			500					505					510			
ctg	tac	tgaggacagc	gggtggaggcc	gaggtggtgg	aggggatgca	ccccagtgtc										2192
Leu	Tyr															


```

cacttttggg cacaggctcc ctccataact gagtggtcca cagatttgca ctacgggttc 2252
tccagctcct ttccaggcag agaggagggg aggtcctgag gggactgctg cccctcactc 2312
ggcatccctt gcagagtcag gactgctccc gggggccagg ctgccctggg aggccccctc 2372
cgagaccagc cagccaggct ctcaggacct gcgctgcctt aggatctttc ttgctgcagc 2432
ctgctccagc ctggccccc a cccagggggc aggcggcccc tcctggcttc tcctgtaggg 2492
cacctccctg cccctagcct cccagcaaat ggtgctctcc tggccctgct ctggcccttc 2552
ccggggccgtg cccctcagcc atgtggcact tctgagctcc tgacctaggc caaggggagg 2612
tctctgcccc ctccccggc cctgggctac ccttgggtcc tgctcctcag gccgctcccc 2672
tgtccctggc catgggtagg agactgcctt ggtcatggcc gcctgcctgt cattcctgac 2732
tcaccaccgt ccccagggtga accattcctc ccttctcctc agctgcagtc gaaggcttta 2792
actttgcaca cttgggatca cagttgcgtc attgtgtatt aaatacttgg aataaatcaa 2852
gcaggt
2858

```

<210> 18
 <211> 514
 <212> PRT
 <213> Homo sapien

<400> 18

Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Gly Tyr Val Pro Glu Asp

1	5	10	15														
Gly	Leu	Thr	Ala	Gln	Gln	Leu	Phe	Ala	Ser	Ala	Asp	Asp	Leu	Thr	Tyr		
		20						25					30				
Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Phe	Ile	Asp	Phe	Ile	Ala	Asp	Glu		
	35						40					45					
Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Arg	Lys	Ile	Thr	Leu	Lys	Thr	Pro		
	50					55					60						
Leu	Ile	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Asp	Met	Ala	Ile		
65					70					75					80		
Ala	Met	Ala	Leu	Met	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr		
			85					90						95			
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Asn	Phe	Glu	Gln		
			100					105						110			
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Ser	His	Thr	Val	Gly		
	115						120					125					
Asp	Val	Leu	Glu	Ala	Lys	Met	Arg	His	Gly	Phe	Ser	Gly	Ile	Pro	Ile		
	130					135					140						
Thr	Glu	Thr	Gly	Thr	Met	Gly	Ser	Lys	Leu	Val	Gly	Ile	Val	Thr	Ser		
145					150						155				160		
Arg	Asp	Ile	Asp	Phe	Leu	Ala	Glu	Lys	Asp	His	Thr	Thr	Leu	Leu	Ser		
			165					170						175			
Glu	Val	Met	Thr	Pro	Arg	Ile	Glu	Leu	Val	Val	Ala	Pro	Ala	Gly	Val		
			180					185					190				
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys		
	195					200						205					
Leu	Pro	Ile	Val	Asn	Asp	Cys	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg		
	210				215						220						
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ser		
225					230					235					240		
Gln	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Val	Gly	Thr	Arg	Glu	Asp	Asp		
			245						250					255			
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Thr	Gln	Ala	Gly	Val	Asp	Val	Ile	Val		
			260					265					270				
Phe	His	Ser	Ser	Gln	Gly	Asn	Ser	Val	Tyr	Gln	Ile	Ala	Met	Val	His		
	275						280					285					
Tyr	Ile	Lys	Gln	Lys	Tyr	Pro	His	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val		
	290				295						300						
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Gly		
305					310					315					320		
Leu	Arg	Val	Gly	Met	Gly	Cys	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val		
			325					330						335			
Met	Ala	Cys	Gly	Arg	Pro	Gln	Gly	Thr	Ala	Val	Tyr	Lys	Val	Ala	Glu		
			340					345					350				
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Ile	Ile	Ala	Asp	Gly	Gly	Ile	Gln		
	355						360					365					


```

Thr Val Gly His Val Val Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
  370          375          380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
385          390          395          400
Phe Phe Ser Asp Gly Val Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
          405          410          415
Leu Asp Pro Met Glu Lys Ser Ser Ser Ser Gln Lys Arg Tyr Phe Ser
          420          425          430
Glu Gly Asp Lys Val Lys Ile Ala Gln Gly Val Ser Gly Ser Ile Gln
          435          440          445
Asp Lys Gly Ser Ile Gln Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
          450          455          460
Gln His Gly Cys Gln Asp Ile Gly Ala Arg Ser Leu Ser Val Leu Arg
465          470          475          480
Ser Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Met Ser
          485          490          495
Pro Gln Ile Glu Gly Gly Val His Gly Leu His Ser Tyr Glu Lys Arg
          500          505          510
Leu Tyr

```

```

<210> 19
<211> 1496
<212> DNA
<213> Homo sapien

```

```

<220>
<221> CDS
<222> (1)...(1188)
<223> Human wild-type Dihydroorotate Dehydrogenase
      (DHODH) "PYRDH" cDNA clone

```

```

<300>
<301> Minet, M., Dufour, M-E., and Lacroute, F.
<302> Cloning and Sequencing of a Human cDNA coding for
<303> Gene (1992)
<304> 121
<306> 393-396

```

```

<400> 19
aaa tta ccg tgg aga cac ctg caa aag cgg gcc cag gat gct gtg atc      48
Lys Leu Pro Trp Arg His Leu Gln Lys Arg Ala Gln Asp Ala Val Ile
  1          5          10          15

atc ctg ggg gga gga gga ctt ctc ttc gcc tcc tac ctg atg gcc acg      96
Ile Leu Gly Gly Gly Gly Leu Leu Phe Ala Ser Tyr Leu Met Ala Thr
          20          25          30

gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act ctg cag ggg      144
Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu Gln Gly
          35          40          45

ctg ctg gac ccg gag tca gcc cac aga ctg gct gtt cgc ttc acc tcc      192
Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser
          50          55          60

ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac atg ctg gaa      240
Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu
          65          70          75          80

gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga att gct gca      288
Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala
          85          90          95

gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat aag atg ggc      336

```

Gly	Phe	Asp	Lys	His	Gly	Glu	Ala	Val	Asp	Gly	Leu	Tyr	Lys	Met	Gly	
			100					105					110			
ttt	ggt	ttt	gtt	gag	ata	gga	agt	gtg	act	cca	aaa	cct	cag	gaa	gga	384
Phe	Gly	Phe	Val	Glu	Ile	Gly	Ser	Val	Thr	Pro	Lys	Pro	Gln	Glu	Gly	
		115					120					125				
aac	cct	aga	ccc	aga	gtc	ttc	cgc	ctc	cct	gag	gac	caa	gct	gtc	att	432
Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Glu	Asp	Gln	Ala	Val	Ile	
	130					135					140					
aac	agg	tat	gga	ttt	aac	agt	cac	ggg	ctt	tca	gtg	gtg	gaa	cac	agg	480
Asn	Arg	Tyr	Gly	Phe	Asn	Ser	His	Gly	Leu	Ser	Val	Val	Glu	His	Arg	
145					150					155					160	
tta	cgg	gcc	aga	cag	cag	aag	cag	gcc	aag	ctc	aca	gaa	gat	gga	ctg	528
Leu	Arg	Ala	Arg	Gln	Gln	Lys	Gln	Ala	Lys	Leu	Thr	Glu	Asp	Gly	Leu	
				165					170					175		
cct	ctg	ggg	gtc	aac	ttg	ggg	aag	aac	aag	acc	tca	gtg	gac	gcc	gcg	576
Pro	Leu	Gly	Val	Asn	Leu	Gly	Lys	Asn	Lys	Thr	Ser	Val	Asp	Ala	Ala	
			180					185					190			
gag	gac	tac	gca	gaa	ggg	gtg	cgc	gta	ctg	ggc	ccc	ctg	gcc	gac	tac	624
Glu	Asp	Tyr	Ala	Glu	Gly	Val	Arg	Val	Leu	Gly	Pro	Leu	Ala	Asp	Tyr	
		195					200					205				
ctg	gtg	gtg	aat	gtg	tcc	agc	ccc	aac	act	gcc	ggg	ctg	cgg	agc	ctt	672
Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu	Arg	Ser	Leu	
	210					215					220					
cag	gga	aag	gcc	gag	ctg	cgc	cgc	ctg	ctg	acc	aag	gtg	ctg	cag	gag	720
Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val	Leu	Gln	Glu	
225					230					235					240	
agg	gat	ggc	ttg	cgg	aga	gtg	cac	agg	ccg	gca	gtc	ctg	gtg	aag	atc	768
Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu	Val	Lys	Ile	
				245					250					255		
gct	cct	gac	ctc	acc	agc	cag	gat	aag	gag	gac	att	gcc	agt	gtg	gtc	816
Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala	Ser	Val	Val	
			260					265					270			
aaa	gag	ttg	ggc	atc	gat	ggg	ctg	att	gtt	acg	aac	acc	acc	gtg	agt	864
Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr	Thr	Val	Ser	
		275					280					285				
cgc	cct	gcg	ggc	ctc	cag	ggg	gcc	ctg	cgc	tct	gaa	aca	gga	ggg	ctg	912
Arg	Pro	Ala	Gly	Leu	Gln	Gly	Ala	Leu	Arg	Ser	Glu	Thr	Gly	Gly	Leu	
	290					295					300					
agt	ggg	aag	ccc	ctc	cgg	gat	tta	tca	act	caa	acc	att	cgg	gag	atg	960
Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile	Arg	Glu	Met	
305					310					315					320	
tat	gca	ctc	acc	caa	ggc	cga	gtt	ccc	ata	att	ggg	gtt	ggt	ggt	gtg	1008
Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val	Gly	Gly	Val	
				325					330					335		
agc	agc	ggg	cag	gac	gcg	ctg	gag	aag	atc	cgg	gca	ggg	gcc	tcc	ctg	1056
Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly	Ala	Ser	Leu	
			340					345					350			
gtg	cag	ctg	tac	acg	gcc	ctc	acc	ttc	tgg	ggg	cca	ccc	gtt	gtg	ggc	1104
Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro	Val	Val	Gly	

```

          355          360          365
aaa gtc aag cgg gaa ctg gag gcc ctt ctg aaa gag cag ggc ttt ggc      1152
Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly Phe Gly
      370          375          380

gga gtc aca gat gcc att gga gca gat cat cgg agg tgaggacagc      1198
Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
      385          390          395

gtctgacggg aagcctgata tggaaccttc ccaaggactc aggcaagcct ttgtggctgg      1258
atcatgagag gagggactcc atcttgagcc atgtcccccga gcctggcatg cgtgcactgt      1318
aaacgccaat cgggggggtca ccaggatcaa ccgcaggctt tcttcagtcc cttgggtcaga      1378
ccataaactg catttttgat tctttgtgga ttcaaaccct aggatccatc agtcttgcaa      1438
ggacattgaa tattaggagg aaaaagtcac ggaaaaaata aagccattta gaacctgg      1496

<210> 20
<211> 396
<212> PRT
<213> Homo Sapien

```

```

<400> 20
Lys Leu Pro Trp Arg His Leu Gln Lys Arg Ala Gln Asp Ala Val Ile
 1      5      10      15
Ile Leu Gly Gly Gly Gly Leu Leu Phe Ala Ser Tyr Leu Met Ala Thr
      20      25      30
Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu Gln Gly
      35      40      45
Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser
      50      55      60
Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu
      65      70      75      80
Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala
      85      90      95
Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys Met Gly
      100      105      110
Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln Glu Gly
      115      120      125
Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala Val Ile
      130      135      140
Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu His Arg
      145      150      155      160
Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu Asp Gly Leu
      165      170      175
Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp Ala Ala
      180      185      190
Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala Asp Tyr
      195      200      205
Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg Ser Leu
      210      215      220
Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu Gln Glu
      225      230      235      240
Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val Lys Ile
      245      250      255
Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser Val Val
      260      265      270
Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr Val Ser
      275      280      285
Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly Gly Leu
      290      295      300
Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg Glu Met
      305      310      315      320
Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly Gly Val
      325      330      335
Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala Ser Leu

```

```

          340          345          350
Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val Val Gly
          355          360          365
Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly Phe Gly
          370          375          380
Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
385          390          395

```

<210> 21
 <211> 1101
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)...(1101)
 <223> DHODH Truncated 39 kDa Construct

<300>
 <301> Copeland, R.A., et al.
~~<302> Recombinant Human Dihydroorotate Dehydrogenase~~
 <303> Arch. Biochem. Biophys. (1995)
 <304> 323
 <306> 79-86

```

<400> 21
atg gcc acg gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act      48
Met Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr
  1          5          10          15

ctg cag ggg ctg ctg gac ccg gag tca gcc cac aga ctg gct gtt cgc      96
Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg
          20          25          30

ttc acc tcc ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac      144
Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp
          35          40          45

atg ctg gaa gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga      192
Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly
          50          55          60

att gct gca gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat      240
Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr
          65          70          75

aag atg ggc ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct      288
Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro
          85          90          95

cag gaa gga aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa      336
Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln
          100          105          110

gct gtc att aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg      384
Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val
          115          120          125

gaa cac agg tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa      432
Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu
          130          135          140

gat gga ctg cct ctg ggg gtc aac ttg ggg aag aac aag acc tca gtg      480
Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val
145          150          155          160

```

gac gcc gcg gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu 165 170 175	528
gcc gac tac ctg gtg gtg aat gtg tcc agc ccc aac act gcc ggg ctg Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu 180 185 190	576
cgg agc ctt cag gga aag gcc gag ctg cgc cgc ctg ctg acc aag gtg Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val 195 200 205	624
ctg cag gag agg gat ggc ttg cgg aga gtg cac agg ccg gca gtc ctg Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu 210 215 220	672
gtg aag atc gct cct gac ctc acc agc cag gat aag gag gac att gcc Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala 225 230 235 240	720
agt gtg gtc aaa gag ttg ggc atc gat ggg ctg att gtt acg aac acc Ser Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr 245 250 255	768
acc gtg agt cgc cct gcg ggc ctc cag ggt gcc ctg cgc tct gaa aca Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr 260 265 270	816
gga ggg ctg agt ggg aag ccc ctc cgg gat tta tca act caa acc att Gly Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile 275 280 285	864
cgg gag atg tat gca ctc acc caa ggc cga gtt ccc ata att ggg gtt Arg Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val 290 295 300	912
ggt ggt gtg agc agc ggg cag gac gcg ctg gag aag atc cgg gca ggg Gly Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly 305 310 315 320	960
gcc tcc ctg gtg cag ctg tac acg gcc ctc acc ttc tgg ggg cca ccc Ala Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro 325 330 335	1008
gtt gtg ggc aaa gtc aag cgg gaa ctg gag gcc ctt ctg aaa gag cag Val Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln 340 345 350	1056
ggc ttt ggc gga gtc aca gat gcc att gga gca gat cat cgg agg Gly Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg 355 360 365	1101

<210> 22
 <211> 367
 <212> PRT
 <213> Homo sapien

<400> 22
 Met Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr
 1 5 10 15
 Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg
 20 25 30
 Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp

		35				40				45							
Met	Leu	Glu	Val	Arg	Val	Leu	Gly	His	Lys	Phe	Arg	Asn	Pro	Val	Gly		
	50					55					60						
Ile	Ala	Ala	Gly	Phe	Asp	Lys	His	Gly	Glu	Ala	Val	Asp	Gly	Leu	Tyr		
65					70					75					80		
Lys	Met	Gly	Phe	Gly	Phe	Val	Glu	Ile	Gly	Ser	Val	Thr	Pro	Lys	Pro		
				85					90					95			
Gln	Glu	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Glu	Asp	Gln		
			100					105					110				
Ala	Val	Ile	Asn	Arg	Tyr	Gly	Phe	Asn	Ser	His	Gly	Leu	Ser	Val	Val		
		115				120						125					
Glu	His	Arg	Leu	Arg	Ala	Arg	Gln	Gln	Lys	Gln	Ala	Lys	Leu	Thr	Glu		
	130					135					140						
Asp	Gly	Leu	Pro	Leu	Gly	Val	Asn	Leu	Gly	Lys	Asn	Lys	Thr	Ser	Val		
145					150					155					160		
Asp	Ala	Ala	Glu	Asp	Tyr	Ala	Glu	Gly	Val	Arg	Val	Leu	Gly	Pro	Leu		
				165					170					175			
Ala	Asp	Tyr	Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu		
			180					185					190				
Arg	Ser	Leu	Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val		
		195				200					205						
Leu	Gln	Glu	Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu		
	210					215					220						
Val	Lys	Ile	Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala		
225					230					235					240		
Ser	Val	Val	Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr		
				245					250					255			
Thr	Val	Ser	Arg	Pro	Ala	Gly	Leu	Gln	Gly	Ala	Leu	Arg	Ser	Glu	Thr		
			260					265					270				
Gly	Gly	Leu	Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile		
		275				280						285					
Arg	Glu	Met	Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val		
	290					295				300							
Gly	Gly	Val	Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly		
305					310					315					320		
Ala	Ser	Leu	Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro		
				325				330					335				
Val	Val	Gly	Lys	Val	Lys	Arg	Glu	Leu	Glu	Ala	Leu	Leu	Lys	Glu	Gln		
			340					345					350				
Gly	Phe	Gly	Gly	Val	Thr	Asp	Ala	Ile	Gly	Ala	Asp	His	Arg	Arg			
		355				360					365						

<210> 23
 <211> 1101
 <212> DNA
 <213> Homo sapien

<220>
 <221> mutation
 <222> 79
 <223> C to G mutation

<221> mutation
 <222> 80
 <223> A to C mutation

<221> CDS
 <222> (4)...(1101)
 <223> His26Ala DHODH mutant

<300>
 <301> Davis et al.
 <302> Histidine to Alanine mutants of Human Dihydroorota
 <303> Biochem. Pharmacol. (1997)
 <304> 54

<306> 459-465

<400> 23

atg gcc acg gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act	48
Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr	
1 5 10 15	
ctg cag ggg ctg ctg gac ccg gag tca gcc gcc aga ctg gct gtt cgc	96
Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala Ala Arg Leu Ala Val Arg	
20 25 30	
ttc acc tcc ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac	144
Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp	
35 40 45	
atg ctg gaa gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga	192
Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly	
50 55 60	
att gct gca gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat	240
Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr	
65 70 75	
aag atg ggc ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct	288
Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro	
80 85 90 95	
cag gaa gga aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa	336
Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln	
100 105 110	
gct gtc att aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg	384
Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val	
115 120 125	
gaa cac agg tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa	432
Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu	
130 135 140	
gat gga ctg cct ctg ggg gtc aac ttg ggg aag aac aag acc tca gtg	480
Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val	
145 150 155	
gac gcc gcg gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg	528
Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu	
160 165 170 175	
gcc gac tac ctg gtg gtg aat gtg tcc agc ccc aac act gcc ggg ctg	576
Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu	
180 185 190	
cgg agc ctt cag gga aag gcc gag ctg cgc cgc ctg ctg acc aag gtg	624
Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val	
195 200 205	
ctg cag gag agg gat ggc ttg cgg aga gtg cac agg ccg gca gtc ctg	672
Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu	
210 215 220	
gtg aag atc gct cct gac ctc acc agc cag gat aag gag gac att gcc	720
Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala	
225 230 235	
agt gtg gtc aaa gag ttg ggc atc gat ggg ctg att gtt acg aac acc	768
Ser Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr	

240	245	250	255	
acc gtg agt cgc cct gcg ggc ctc cag ggt gcc ctg cgc tct gaa aca				816
Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr				
	260	265	270	
gga ggg ctg agt ggg aag ccc ctc cgg gat tta tca act caa acc att				864
Gly Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile				
	275	280	285	
cgg gag atg tat gca ctc acc caa ggc cga gtt ccc ata att ggg gtt				912
Arg Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val				
	290	295	300	
ggt ggt gtg agc agc ggg cag gac gcg ctg gag aag atc cgg gca ggg				960
Gly Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly				
	305	310	315	
gcc tcc ctg gtg cag ctg tac acg gcc ctc acc ttc tgg ggg cca ccc				1008
Ala Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro				
	320	325	330	335
ggt gtg ggc aaa gtc aag cgg gaa ctg gag gcc ctt ctg aaa gag cag				1056
Val Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln				
	340	345	350	
ggc ttt ggc gga gtc aca gat gcc att gga gca gat cat cgg agg				1101
Gly Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg				
	355	360	365	

<210> 24
 <211> 366
 <212> PRT
 <213> Homo sapien

<400> 24
 Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu
 1 5 10 15
 Gln Gly Leu Leu Asp Pro Glu Ser Ala Ala Arg Leu Ala Val Arg Phe
 20 25 30
 Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met
 35 40 45
 Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile
 50 55 60
 Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys
 65 70 75 80
 Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln
 85 90 95
 Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala
 100 105 110
 Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu
 115 120 125
 His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu Asp
 130 135 140
 Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp
 145 150 155 160
 Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala
 165 170 175
 Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg
 180 185 190
 Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu
 195 200 205
 Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val
 210 215 220


```

Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser
225      230      235      240
Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr
      245      250      255
Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly
      260      265      270
Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg
      275      280      285
Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly
      290      295      300
Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala
305      310      315      320
Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val
      325      330      335
Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly
      340      345      350
Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
      355      360      365

```

<210> 25

<211> 1560

<212> DNA

<213> Aspergillus nidulans

<220>

<221> CDS

<222> (1)...(1560)

<223> Aspergillus nidulans Val200Glu mutant DHODH cDNA

<221> mutation

<222> 599

<223> T to A mutataation

<400> 25

```

atg gct acg aat tct ttc cga aaa ctc act ttt tca gga gcc tcc cgt      48
Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg
 1              5              10              15

ctg ggt ggt tgt cgc cgt ctc cca cta acc tgc aga caa ctt cga ttc      96
Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe
      20              25              30

gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa      144
Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
      35              40              45

tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag      192
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
      50              55              60

gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg      240
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
      65              70              75              80

acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg      288
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
      85              90              95

cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg      336
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
      100              105              110

gaa gat gcg cat cat att ggt gtc gat act tta aag atg ctg tat aag      384
Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
      115              120              125

```

tat Tyr	ggt Gly	ctg Leu	cat His	cca Pro	agg Arg	gaa Glu	cgg Arg	ggg Gly	gat Asp	ccg Pro	gat Asp	gga Gly	gat Asp	ggg Gly	gcg Ala	432
	130					135				140						
ctg Leu	gcg Ala	aca Thr	gag Glu	gtc Val	ttt Phe	ggg Gly	tat Tyr	aca Thr	ctg Leu	tca Ser	aac Asn	cca Pro	att Ile	ggc Gly	ata Ile	480
	145				150					155					160	
tcg Ser	ggc Gly	ggc Gly	ctg Leu	gac Asp	aag Lys	cat His	gct Ala	gag Glu	atc Ile	cct Pro	gat Asp	ccg Pro	ctg Leu	ttc Phe	gcg Ala	528
				165					170					175		
atc Ile	ggt Gly	cct Pro	gcc Ala	att Ile	gtc Val	gaa Glu	gtc Val	ggg Gly	ggg Gly	acg Thr	aca Thr	ccc Pro	tta Leu	cca Pro	cag Gln	576
			180					185					190			
gat Asp	ggt Gly	aac Asn	ccg Pro	cgt Arg	cct Pro	cgc Arg	gaa Glu	ttc Phe	cga Arg	ctt Leu	cca Pro	tca Ser	cag Gln	aga Arg	gcg Ala	624
		195					200					205				
atg Met	ata Ile	aac Asn	cgg Arg	tac Tyr	ggc Gly	ctc Leu	aac Asn	tcc Ser	aaa Lys	ggc Gly	gca Ala	gat Asp	cac His	atg Met	gca Ala	672
	210					215					220					
gct Ala	atc Ile	ttg Leu	gag Glu	caa Gln	cga Arg	gta Val	cgc Arg	gat Asp	ttt Phe	gcc Ala	tac Tyr	gca Ala	aac Asn	gga Gly	ttt Phe	720
	225				230					235					240	
ggg Gly	gca Ala	tac Tyr	gat Asp	gcg Ala	gct Ala	aag Lys	cag Gln	cgt Arg	gta Val	ttg Leu	gac Asp	ggc Gly	gaa Glu	gct Ala	ggg Gly	768
				245				250						255		
gtg Val	cca Pro	cca Pro	ggt Gly	agt Ser	ctt Leu	cag Gln	cct Pro	ggt Gly	aag Lys	ctt Leu	tta Leu	gct Ala	gtc Val	caa Gln	gtg Val	816
			260					265					270			
gca Ala	aag Lys	aac Asn	aag Lys	gcc Ala	act Thr	cct Pro	gac Asp	ggc Gly	gac Asp	att Ile	gaa Glu	gcc Ala	atc Ile	aag Lys	cgc Arg	864
		275					280					285				
gac Asp	tat Tyr	gtg Val	tat Tyr	tgc Cys	gtg Val	gac Asp	cgt Arg	gtg Val	gcc Ala	aaa Lys	tac Tyr	gct Ala	gat Asp	att Ile	ctt Leu	912
	290					295					300					
gtt Val	gtg Val	aat Asn	gta Val	tcg Ser	agc Ser	ccc Pro	aac Asn	aca Thr	ccc Pro	ggg Gly	ctc Leu	cgt Arg	gac Asp	ctt Leu	caa Gln	960
	305				310					315					320	
gcc Ala	act Thr	gcc Ala	ccg Pro	ctc Leu	aca Thr	gct Ala	atc Ile	ttg Leu	agt Ser	gct Ala	gtc Val	gtt Val	ggc Gly	gcg Ala	gca Ala	1008
				325				330						335		
aag Lys	agc Ser	gtg Val	aac Asn	cgc Arg	aag Lys	acc Thr	aaa Lys	cca Pro	tat Tyr	gtt Val	atg Met	gtc Val	aag Lys	gtc Val	agt Ser	1056
			340					345					350			
ccg Pro	gat Asp	gaa Glu	gac Asp	tca Ser	gat Asp	gaa Glu	caa Gln	gtc Val	tct Ser	ggg Gly	atc Ile	tgc Cys	gac Asp	gcc Ala	gtc Val	1104
		355					360					365				
cga Arg	gca Ala	tcc Ser	ggt Gly	gtc Val	gac Asp	gga Gly	gtg Val	att Ile	gtc Val	gga Gly	aac Asn	aca Thr	aca Thr	aac Asn	cgt Arg	1152
	370					375					380					

cgc	ccc	gac	cct	ata	ccc	caa	ggt	tac	act	ctt	ccg	gcc	aag	gag	cag	1200
Arg	Pro	Asp	Pro	Ile	Pro	Gln	Gly	Tyr	Thr	Leu	Pro	Ala	Lys	Glu	Gln	
385					390					395					400	
gca	acg	ttg	aaa	gaa	acc	ggc	ggg	tat	tca	ggt	cca	cag	ctg	ttc	gat	1248
Ala	Thr	Leu	Lys	Glu	Thr	Gly	Gly	Tyr	Ser	Gly	Pro	Gln	Leu	Phe	Asp	
				405				410						415		
cgc	aca	gtg	gcc	ctt	gtg	gct	cgg	tac	cgc	tcc	atg	ctg	gat	gcg	gag	1296
Arg	Thr	Val	Ala	Leu	Val	Ala	Arg	Tyr	Arg	Ser	Met	Leu	Asp	Ala	Glu	
			420					425					430			
tcg	gaa	acg	gcc	gga	tcc	gcc	aag	gat	tca	gca	gcg	acc	ata	gcg	caa	1344
Ser	Glu	Thr	Ala	Gly	Ser	Ala	Lys	Asp	Ser	Ala	Ala	Thr	Ile	Ala	Gln	
		435					440					445				
aca	gag	cca	ggc	tcg	gaa	aac	gtt	cct	cct	gtg	gaa	gcg	cca	agc	gga	1392
Thr	Glu	Pro	Gly	Ser	Glu	Asn	Val	Pro	Pro	Val	Glu	Ala	Pro	Ser	Gly	
	450					455					460					

ctg	ccg	cgc	aaa	gtt	atc	ttc	gct	tcg	ggt	ggg	atc	acc	aac	ggg	aag	1440
Leu	Pro	Arg	Lys	Val	Ile	Phe	Ala	Ser	Gly	Gly	Ile	Thr	Asn	Gly	Lys	
465					470				475						480	
cag	gct	cac	gct	gtt	tta	gac	aca	ggg	gca	tct	gtt	gcc	atg	atg	tac	1488
Gln	Ala	His	Ala	Val	Leu	Asp	Thr	Gly	Ala	Ser	Val	Ala	Met	Met	Tyr	
				485				490						495		
acc	ggt	gtg	gtc	tat	ggg	ggc	gtc	ggc	act	gtc	act	cga	gtg	aag	caa	1536
Thr	Gly	Val	Val	Tyr	Gly	Gly	Val	Gly	Thr	Val	Thr	Arg	Val	Lys	Gln	
			500					505					510			
gaa	ctt	cga	acg	gcg	aaa	aag	gag									1560
Glu	Leu	Arg	Thr	Ala	Lys	Lys	Glu									
		515					520									

<210> 26
 <211> 520
 <212> PRT
 <213> Aspergillus nidulans

<400> 26
 Met Ala Thr Asn Ser Phe Arg Lys Leu Thr Phe Ser Gly Ala Ser Arg
 1 5 10 15
 Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe
 20 25 30
 Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu
 35 40 45
 Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys
 50 55 60
 Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
 65 70 75 80
 Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
 85 90 95
 His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
 100 105 110
 Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
 115 120 125
 Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala
 130 135 140
 Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile
 145 150 155 160
 Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala
 165 170 175

Ile	Gly	Pro	Ala	Ile	Val	Glu	Val	Gly	Gly	Thr	Thr	Pro	Leu	Pro	Gln
			180					185					190		
Asp	Gly	Asn	Pro	Arg	Pro	Arg	Glu	Phe	Arg	Leu	Pro	Ser	Gln	Arg	Ala
		195					200					205			
Met	Ile	Asn	Arg	Tyr	Gly	Leu	Asn	Ser	Lys	Gly	Ala	Asp	His	Met	Ala
	210				215					220					
Ala	Ile	Leu	Glu	Gln	Arg	Val	Arg	Asp	Phe	Ala	Tyr	Ala	Asn	Gly	Phe
225				230					235						240
Gly	Ala	Tyr	Asp	Ala	Ala	Lys	Gln	Arg	Val	Leu	Asp	Gly	Glu	Ala	Gly
			245					250						255	
Val	Pro	Pro	Gly	Ser	Leu	Gln	Pro	Gly	Lys	Leu	Leu	Ala	Val	Gln	Val
			260					265					270		
Ala	Lys	Asn	Lys	Ala	Thr	Pro	Asp	Gly	Asp	Ile	Glu	Ala	Ile	Lys	Arg
		275					280					285			
Asp	Tyr	Val	Tyr	Cys	Val	Asp	Arg	Val	Ala	Lys	Tyr	Ala	Asp	Ile	Leu
	290					295					300				
Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly	Leu	Arg	Asp	Leu	Gln
305				310						315					320
Ala	Thr	Ala	Pro	Leu	Thr	Ala	Ile	Leu	Ser	Ala	Val	Val	Gly	Ala	Ala
			325					330						335	

Lys	Ser	Val	Asn	Arg	Lys	Thr	Lys	Pro	Tyr	Val	Met	Val	Lys	Val	Ser
			340					345					350		
Pro	Asp	Glu	Asp	Ser	Asp	Glu	Gln	Val	Ser	Gly	Ile	Cys	Asp	Ala	Val
		355				360						365			
Arg	Ala	Ser	Gly	Val	Asp	Gly	Val	Ile	Val	Gly	Asn	Thr	Thr	Asn	Arg
	370				375						380				
Arg	Pro	Asp	Pro	Ile	Pro	Gln	Gly	Tyr	Thr	Leu	Pro	Ala	Lys	Glu	Gln
385				390						395					400
Ala	Thr	Leu	Lys	Glu	Thr	Gly	Gly	Tyr	Ser	Gly	Pro	Gln	Leu	Phe	Asp
			405					410						415	
Arg	Thr	Val	Ala	Leu	Val	Ala	Arg	Tyr	Arg	Ser	Met	Leu	Asp	Ala	Glu
			420					425					430		
Ser	Glu	Thr	Ala	Gly	Ser	Ala	Lys	Asp	Ser	Ala	Ala	Thr	Ile	Ala	Gln
		435				440						445			
Thr	Glu	Pro	Gly	Ser	Glu	Asn	Val	Pro	Pro	Val	Glu	Ala	Pro	Ser	Gly
	450					455					460				
Leu	Pro	Arg	Lys	Val	Ile	Phe	Ala	Ser	Gly	Gly	Ile	Thr	Asn	Gly	Lys
465				470						475					480
Gln	Ala	His	Ala	Val	Leu	Asp	Thr	Gly	Ala	Ser	Val	Ala	Met	Met	Tyr
			485					490					495		
Thr	Gly	Val	Val	Tyr	Gly	Gly	Val	Gly	Thr	Val	Thr	Arg	Val	Lys	Gln
		500						505					510		
Glu	Leu	Arg	Thr	Ala	Lys	Lys	Glu								
		515					520								

<210> 27

<211> 1560

<212> DNA

<213> Aspergillus nidulans

<220>

<221> CDS

<222> (1)...(1560)

<223> Aspergillus nidulans Ala115Val mutant DHODH cDNA

<221> mutation

<222> 344

<223> C to T mutation

<400> 27

atg	gct	acg	aat	tct	ttc	cga	aaa	ctc	act	ttt	tca	gga	gcc	tcc	cgt
Met	Ala	Thr	Asn	Ser	Phe	Arg	Lys	Leu	Thr	Phe	Ser	Gly	Ala	Ser	Arg
1				5				10						15	

48

ctg	ggg	ggg	tgt	cgc	cgt	ctc	cca	cta	acc	tgc	aga	caa	ctt	cga	ttc
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

96

Leu	Gly	Gly	Cys 20	Arg	Arg	Leu	Pro	Leu 25	Thr	Cys	Arg	Gln	Leu 30	Arg	Phe	
gcc	tcc	gac	agc	gga	gcc	gca	gcg	gca	act	aca	aaa	gca	acg	gcc	gaa	144
Ala	Ser	Asp	Ser	Gly	Ala	Ala	Ala	Ala	Thr	Thr	Lys	Ala	Thr	Ala	Glu	
		35					40					45				
tca	gca	gcc	gag	tca	gct	agt	ata	aac	gtc	aaa	gag	gca	ccc	aaa	aag	192
Ser	Ala	Ala	Glu	Ser	Ala	Ser	Ile	Asn	Val	Lys	Glu	Ala	Pro	Lys	Lys	
	50					55					60					
gcc	gga	cgg	ggc	ctg	cgg	cgc	acg	gtc	ctg	gga	acg	tcg	ttg	gcg	ctg	240
Ala	Gly	Arg	Gly	Leu	Arg	Arg	Thr	Val	Leu	Gly	Thr	Ser	Leu	Ala	Leu	
65					70					75					80	
acg	ctg	ctg	gtt	gga	tat	gtc	tac	ggg	acg	gac	acc	cgg	gcg	agt	gtg	288
Thr	Leu	Leu	Val	Gly	Tyr	Val	Tyr	Gly	Thr	Asp	Thr	Arg	Ala	Ser	Val	
			85						90					95		
cat	cgg	tac	ggt	gtt	gtg	cgg	ctg	att	aga	gca	ttg	tat	cct	gat	gcg	336
His	Arg	Tyr	Gly	Val	Val	Pro	Leu	Ile	Arg	Ala	Leu	Tyr	Pro	Asp	Ala	
			100					105					110			
gaa	gat	gtg	cat	cat	att	ggt	gtc	gat	act	tta	aag	atg	ctg	tat	aag	384
Glu	Asp	Val	His	His	Ile	Gly	Val	Asp	Thr	Leu	Lys	Met	Leu	Tyr	Lys	
		115					120					125				
tat	ggt	ctg	cat	cca	agg	gaa	cgg	ggg	gat	cgg	gat	gga	gat	ggg	gcg	432
Tyr	Gly	Leu	His	Pro	Arg	Glu	Arg	Gly	Asp	Pro	Asp	Gly	Asp	Gly	Ala	
	130					135					140					
ctg	gcg	aca	gag	gtc	ttt	ggg	tat	aca	ctg	tca	aac	cca	att	ggc	ata	480
Leu	Ala	Thr	Glu	Val	Phe	Gly	Tyr	Thr	Leu	Ser	Asn	Pro	Ile	Gly	Ile	
145					150					155					160	
tcg	ggc	ggc	ctg	gac	aag	cat	gct	gag	atc	cct	gat	cgg	ctg	ttc	gcg	528
Ser	Gly	Gly	Leu	Asp	Lys	His	Ala	Glu	Ile	Pro	Asp	Pro	Leu	Phe	Ala	
				165					170					175		
atc	ggt	cct	gcc	att	gtc	gaa	gtc	ggg	ggt	acg	aca	ccc	tta	cca	cag	576
Ile	Gly	Pro	Ala	Ile	Val	Glu	Val	Gly	Gly	Thr	Thr	Pro	Leu	Pro	Gln	
			180					185					190			
gat	ggt	aac	cgg	cgt	cct	cgc	gta	ttc	cga	ctt	cca	tca	cag	aga	gcg	624
Asp	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Ser	Gln	Arg	Ala	
		195					200					205				
atg	ata	aac	cgg	tac	ggc	ctc	aac	tcc	aaa	ggc	gca	gat	cac	atg	gca	672
Met	Ile	Asn	Arg	Tyr	Gly	Leu	Asn	Ser	Lys	Gly	Ala	Asp	His	Met	Ala	
	210					215					220					
gct	atc	ttg	gag	caa	cga	gta	cgc	gat	ttt	gcc	tac	gca	aac	gga	ttt	720
Ala	Ile	Leu	Glu	Gln	Arg	Val	Arg	Asp	Phe	Ala	Tyr	Ala	Asn	Gly	Phe	
225					230					235					240	
ggg	gca	tac	gat	gcg	gct	aag	cag	cgt	gta	ttg	gac	ggc	gaa	gct	ggt	768
Gly	Ala	Tyr	Asp	Ala	Ala	Lys	Gln	Arg	Val	Leu	Asp	Gly	Glu	Ala	Gly	
				245					250					255		
gtg	cca	cca	ggt	agt	ctt	cag	cct	ggt	aag	ctt	tta	gct	gtc	caa	gtg	816
Val	Pro	Pro	Gly	Ser	Leu	Gln	Pro	Gly	Lys	Leu	Leu	Ala	Val	Gln	Val	
			260					265					270			
gca	aag	aac	aag	gcc	act	cct	gac	ggc	gac	att	gaa	gcc	atc	aag	cgc	864
Ala	Lys	Asn	Lys	Ala	Thr	Pro	Asp	Gly	Asp	Ile	Glu	Ala	Ile	Lys	Arg	

275						280						285						
gac	tat	gtg	tat	tgc	gtg	gac	cgt	gtg	gcc	aaa	tac	gct	gat	att	ctt			912
Asp	Tyr	Val	Tyr	Cys	Val	Asp	Arg	Val	Ala	Lys	Tyr	Ala	Asp	Ile	Leu			
	290						295				300							
ggt	gtg	aat	gta	tcg	agc	ccc	aac	aca	ccc	ggg	ctc	cgt	gac	ctt	caa			960
Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly	Leu	Arg	Asp	Leu	Gln			
	305				310					315					320			
gcc	act	gcc	ccg	ctc	aca	gct	atc	ttg	agt	gct	gtc	ggt	ggc	gcg	gca			1008
Ala	Thr	Ala	Pro	Leu	Thr	Ala	Ile	Leu	Ser	Ala	Val	Val	Gly	Ala	Ala			
				325					330					335				
aag	agc	gtg	aac	cgc	aag	acc	aaa	cca	tat	ggt	atg	gtc	aag	gtc	agt			1056
Lys	Ser	Val	Asn	Arg	Lys	Thr	Lys	Pro	Tyr	Val	Met	Val	Lys	Val	Ser			
			340					345					350					
ccg	gat	gaa	gac	tca	gat	gaa	caa	gtc	tct	ggg	atc	tgc	gac	gcc	gtc			1104
Pro	Asp	Glu	Asp	Ser	Asp	Glu	Gln	Val	Ser	Gly	Ile	Cys	Asp	Ala	Val			
		355					360				365							
cga	gca	tcc	ggg	gtc	gac	gga	gtg	att	gtc	gga	aac	aca	aca	aac	cgt			1152
Arg	Ala	Ser	Gly	Val	Asp	Gly	Val	Ile	Val	Gly	Asn	Thr	Thr	Asn	Arg			
	370					375					380							
cgc	ccc	gac	cct	ata	ccc	caa	ggg	tac	act	ctt	ccg	gcc	aag	gag	cag			1200
Arg	Pro	Asp	Pro	Ile	Pro	Gln	Gly	Tyr	Thr	Leu	Pro	Ala	Lys	Glu	Gln			
	385				390					395				400				
gca	acg	ttg	aaa	gaa	acc	ggc	ggg	tat	tca	ggg	cca	cag	ctg	ttc	gat			1248
Ala	Thr	Leu	Lys	Glu	Thr	Gly	Gly	Tyr	Ser	Gly	Pro	Gln	Leu	Phe	Asp			
				405				410						415				
cgc	aca	gtg	gcc	ctt	gtg	gct	cgg	tac	cgc	tcc	atg	ctg	gat	gcg	gag			1296
Arg	Thr	Val	Ala	Leu	Val	Ala	Arg	Tyr	Arg	Ser	Met	Leu	Asp	Ala	Glu			
			420					425					430					
tcg	gaa	acg	gcc	gga	tcc	gcc	aag	gat	tca	gca	gcg	acc	ata	gcg	caa			1344
Ser	Glu	Thr	Ala	Gly	Ser	Ala	Lys	Asp	Ser	Ala	Ala	Thr	Ile	Ala	Gln			
		435					440					445						
aca	gag	cca	ggc	tcg	gaa	aac	ggt	cct	cct	gtg	gaa	gcg	cca	agc	gga			1392
Thr	Glu	Pro	Gly	Ser	Glu	Asn	Val	Pro	Pro	Val	Glu	Ala	Pro	Ser	Gly			
	450					455					460							
ctg	ccg	cgc	aaa	ggt	atc	ttc	gct	tcg	ggg	ggg	atc	acc	aac	ggg	aag			1440
Leu	Pro	Arg	Lys	Val	Ile	Phe	Ala	Ser	Gly	Gly	Ile	Thr	Asn	Gly	Lys			
	465				470					475					480			
cag	gct	cac	gct	ggt	tta	gac	aca	ggg	gca	tct	ggt	gcc	atg	atg	tac			1488
Gln	Ala	His	Ala	Val	Leu	Asp	Thr	Gly	Ala	Ser	Val	Ala	Met	Met	Tyr			
				485				490						495				
acc	ggg	gtg	gtc	tat	ggg	ggc	gtc	ggc	act	gtc	act	cga	gtg	aag	caa			1536
Thr	Gly	Val	Val	Tyr	Gly	Gly	Val	Gly	Thr	Val	Thr	Arg	Val	Lys	Gln			
			500					505					510					
gaa	ctt	cga	acg	gcg	aaa	aag	gag											1560
Glu	Leu	Arg	Thr	Ala	Lys	Lys	Glu											
		515					520											

<210> 28
 <211> 520

<212> PRT

<213> Aspergillus nidulans

<400> 28

Met	Ala	Thr	Asn	Ser	Phe	Arg	Lys	Leu	Thr	Phe	Ser	Gly	Ala	Ser	Arg
1				5					10					15	
Leu	Gly	Gly	Cys	Arg	Arg	Leu	Pro	Leu	Thr	Cys	Arg	Gln	Leu	Arg	Phe
			20					25					30		
Ala	Ser	Asp	Ser	Gly	Ala	Ala	Ala	Ala	Thr	Thr	Lys	Ala	Thr	Ala	Glu
		35				40						45			
Ser	Ala	Ala	Glu	Ser	Ala	Ser	Ile	Asn	Val	Lys	Glu	Ala	Pro	Lys	Lys
	50					55					60				
Ala	Gly	Arg	Gly	Leu	Arg	Arg	Thr	Val	Leu	Gly	Thr	Ser	Leu	Ala	Leu
65					70					75					80
Thr	Leu	Leu	Val	Gly	Tyr	Val	Tyr	Gly	Thr	Asp	Thr	Arg	Ala	Ser	Val
				85					90					95	
His	Arg	Tyr	Gly	Val	Val	Pro	Leu	Ile	Arg	Ala	Leu	Tyr	Pro	Asp	Ala
			100					105					110		
Glu	Asp	Val	His	His	Ile	Gly	Val	Asp	Thr	Leu	Lys	Met	Leu	Tyr	Lys
		115					120					125			
Tyr	Gly	Leu	His	Pro	Arg	Glu	Arg	Gly	Asp	Pro	Asp	Gly	Asp	Gly	Ala
	130					135					140				
Leu	Ala	Thr	Glu	Val	Phe	Gly	Tyr	Thr	Leu	Ser	Asn	Pro	Ile	Gly	Ile
145					150					155					160
Ser	Gly	Gly	Leu	Asp	Lys	His	Ala	Glu	Ile	Pro	Asp	Pro	Leu	Phe	Ala
				165					170					175	
Ile	Gly	Pro	Ala	Ile	Val	Glu	Val	Gly	Gly	Thr	Thr	Pro	Leu	Pro	Gln
			180					185					190		
Asp	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Ser	Gln	Arg	Ala
		195					200					205			
Met	Ile	Asn	Arg	Tyr	Gly	Leu	Asn	Ser	Lys	Gly	Ala	Asp	His	Met	Ala
	210					215					220				
Ala	Ile	Leu	Glu	Gln	Arg	Val	Arg	Asp	Phe	Ala	Tyr	Ala	Asn	Gly	Phe
225					230					235					240
Gly	Ala	Tyr	Asp	Ala	Ala	Lys	Gln	Arg	Val	Leu	Asp	Gly	Glu	Ala	Gly
				245					250					255	
Val	Pro	Pro	Gly	Ser	Leu	Gln	Pro	Gly	Lys	Leu	Leu	Ala	Val	Gln	Val
			260					265					270		
Ala	Lys	Asn	Lys	Ala	Thr	Pro	Asp	Gly	Asp	Ile	Glu	Ala	Ile	Lys	Arg
		275					280					285			
Asp	Tyr	Val	Tyr	Cys	Val	Asp	Arg	Val	Ala	Lys	Tyr	Ala	Asp	Ile	Leu
	290					295					300				
Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly	Leu	Arg	Asp	Leu	Gln
305					310					315					320
Ala	Thr	Ala	Pro	Leu	Thr	Ala	Ile	Leu	Ser	Ala	Val	Val	Gly	Ala	Ala
				325					330					335	
Lys	Ser	Val	Asn	Arg	Lys	Thr	Lys	Pro	Tyr	Val	Met	Val	Lys	Val	Ser
			340					345					350		
Pro	Asp	Glu	Asp	Ser	Asp	Glu	Gln	Val	Ser	Gly	Ile	Cys	Asp	Ala	Val
		355					360					365			
Arg	Ala	Ser	Gly	Val	Asp	Gly	Val	Ile	Val	Gly	Asn	Thr	Thr	Asn	Arg
	370					375					380				
Arg	Pro	Asp	Pro	Ile	Pro	Gln	Gly	Tyr	Thr	Leu	Pro	Ala	Lys	Glu	Gln
385					390					395					400
Ala	Thr	Leu	Lys	Glu	Thr	Gly	Gly	Tyr	Ser	Gly	Pro	Gln	Leu	Phe	Asp
				405					410					415	
Arg	Thr	Val	Ala	Leu	Val	Ala	Arg	Tyr	Arg	Ser	Met	Leu	Asp	Ala	Glu
			420					425					430		
Ser	Glu	Thr	Ala	Gly	Ser	Ala	Lys	Asp	Ser	Ala	Ala	Thr	Ile	Ala	Gln
		435					440					445			
Thr	Glu	Pro	Gly	Ser	Glu	Asn	Val	Pro	Pro	Val	Glu	Ala	Pro	Ser	Gly
	450					455					460				
Leu	Pro	Arg	Lys	Val	Ile	Phe	Ala	Ser	Gly	Gly	Ile	Thr	Asn	Gly	Lys
465					470					475					480
Gln	Ala	His	Ala	Val	Leu	Asp	Thr	Gly	Ala	Ser	Val	Ala	Met	Met	Tyr

Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln
 485 490 495
 500 505 510
 Glu Leu Arg Thr Ala Lys Lys Glu
 515 520

<210> 29
 <211> 1707
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (67)...(1611)
 <223> wild-type IMP dehydrogenase cDNA

<400> 29
 cctctgcggc gcggtcctcg gagcggcgcg gttctcggag ccacgcgtct gtcttcctcc 60
 gtgggtc atg gcg gac tac ctg att agc gga ggc acc tct tac gtg ccg 108
 Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro

gac gac ggg ctc aca gcg cag cag ctc ttc aac tgc ggg gac ggc ctc 156
 Asp Asp Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu
 15 20 25 30

acc tac aat gat ttt ctc att ctt cct ggg tat atc gac ttc act gca 204
 Thr Tyr Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala
 35 40 45

gat cag gtg gac ttg acg tct gct cta act aag aag att aca cta aag 252
 Asp Gln Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys
 50 55 60

acc cca ttg gtt tcc tca ccc atg gac act gtc aca gag gct gga atg 300
 Thr Pro Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met
 65 70 75

gcc atc gcg atg gcg ctt aca gga ggt att ggt ttc atc cac cac aac 348
 Ala Ile Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn
 80 85 90

tgc aca cct gaa ttc cag gcc aat gaa gtt cgg aaa gtg aag aaa tac 396
 Cys Thr Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr
 95 100 105 110

gaa cag gga ttc atc act gac ccc gtg gtc ctt agc ccc aag gat cgt 444
 Glu Gln Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg
 115 120 125

gta cgc gat gtt ttt gag gcc aaa gcc agg cat ggc ttc tgt ggt atc 492
 Val Arg Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile
 130 135 140

ccc atc aca gat aca ggc cgg atg ggg agt cga ttg gtg ggc atc atc 540
 Pro Ile Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile
 145 150 155

tcc tca agg gac att gat ttc ctc aag gag gaa gag cat gac cgg ttc 588
 Ser Ser Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe
 160 165 170

ttg gaa gag atc atg act aag agg gaa gat ttg gtg gtc gcc cct gcc 636
 Leu Glu Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala
 175 180 185 190

ggc	gtc	act	ctg	aaa	gag	gca	aat	gag	att	ctg	cag	cga	agt	aaa	aag	684
Gly	Val	Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	
				195					200					205		
gga	aag	ttg	ccc	att	gtg	aat	gaa	aat	gat	gag	ctg	gta	gcc	atc	att	732
Gly	Lys	Leu	Pro	Ile	Val	Asn	Glu	Asn	Asp	Glu	Leu	Val	Ala	Ile	Ile	
			210					215					220			
gcc	cgg	aca	gac	cta	aag	aag	aat	cgt	gat	tac	ccc	ctg	gcc	tcc	aaa	780
Ala	Arg	Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	
		225					230					235				
gat	gcc	aag	aag	caa	ctg	ctg	tgt	ggg	gca	gcc	att	ggc	act	cat	gag	828
Asp	Ala	Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	
	240					245					250					
gat	gac	aag	tat	agg	ctg	gac	tta	ctg	gcc	ctt	gct	ggc	gtg	gat	gta	876
Asp	Asp	Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Leu	Ala	Gly	Val	Asp	Val	
255					260					265					270	
gtg	gtt	ttg	gac	tct	tcc	cag	gga	aac	tcc	atc	ttc	caa	atc	aat	atg	924
Val	Val	Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	
				275					280					285		
atc	aaa	tac	atc	aag	gag	aag	tat	ccc	agt	cta	cag	gtc	att	gga	ggc	972
Ile	Lys	Tyr	Ile	Lys	Glu	Lys	Tyr	Pro	Ser	Leu	Gln	Val	Ile	Gly	Gly	
			290					295					300			
aat	gta	gtc	act	gct	gcg	caa	gcc	aag	aac	ctc	ata	gat	gca	ggc	gta	1020
Asn	Val	Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	
		305					310					315				
gat	gct	ttg	cga	gtc	ggc	atg	gga	agt	ggc	tcc	atc	tgc	atc	acc	cag	1068
Asp	Ala	Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	
	320					325					330					
gaa	gtg	ttg	gcc	tgt	ggg	cgg	ccc	caa	gcc	aca	gca	gtg	tac	aag	gtc	1116
Glu	Val	Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	
335					340					345					350	
tct	gag	tat	gcc	cgt	cgc	ttt	ggc	gtt	cct	gtt	att	gct	gat	gga	gga	1164
Ser	Glu	Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	
				355					360					365		
atc	caa	aat	gtg	ggc	cat	att	gcc	aaa	gct	ttg	gct	ctt	ggg	gct	tcc	1212
Ile	Gln	Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	
			370					375					380			
aca	gtc	atg	atg	ggc	tcc	ctc	ctg	gct	gcc	acc	act	gag	gcc	cct	ggc	1260
Thr	Val	Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	
		385					390					395				
gag	tac	ttc	ttc	tca	gat	ggg	atc	cgg	ctg	aag	aaa	tac	cga	ggc	atg	1308
Glu	Tyr	Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	
	400					405					410					
ggc	tct	ctt	gat	gcc	atg	gac	aaa	cat	ctc	agc	agc	cag	aac	cga	tac	1356
Gly	Ser	Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	
415					420					425					430	
ttc	agt	gaa	gct	gac	aaa	atc	aaa	gtg	gcc	caa	gga	gtt	tca	ggg	gca	1404
Phe	Ser	Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	
				435					440					445		

```

gtg cag gac aag ggg tct atc cac aag ttc gtt cct tac ctg att gct      1452
Val Gln Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala
      450      455      460

ggc atc cag cat tcc tgt caa gac att ggt gcc aag agt tta acc caa      1500
Gly Ile Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln
      465      470      475

gtc aga gcc atg acg tac tcg ggg gag ctt aaa ttt gag aag agg aca      1548
Val Arg Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr
      480      485      490

tcc tct gct cag gtg gaa ggt ggc gtc cac agc ctc cat tcg tac gag      1596
Ser Ser Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu
      495      500      505      510

aaa cgg ctt ttc tga aaacagatcc agtatatgcc ttgaattttt caataaaagt      1651
Lys Arg Leu Phe *

```

```

ctgggaaaaa aaaagtgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa      1707

```

```

<210> 30
<211> 514
<212> PRT
<213> Mus musculus

```

```

<400> 30
Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
 1      5      10      15
Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
 20      25      30
Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35      40      45
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50      55      60
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
 65      70      75      80
Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85      90      95
Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln
100      105      110
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg
115      120      125
Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
130      135      140
Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
145      150      155      160
Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Arg Phe Leu Glu
165      170      175
Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala Gly Val
180      185      190
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
195      200      205
Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile Ala Arg
210      215      220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
225      230      235      240
Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
245      250      255
Lys Tyr Arg Leu Asp Leu Leu Ala Leu Ala Gly Val Asp Val Val Val
260      265      270
Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
275      280      285
Tyr Ile Lys Glu Lys Tyr Pro Ser Leu Gln Val Ile Gly Gly Asn Val

```

290	295	300
Val Thr Ala Ala Gln	Ala Lys Asn Leu Ile Asp	Ala Gly Val Asp Ala
305	310	315
Leu Arg Val Gly Met	Gly Ser Gly Ser Ile Cys	Ile Thr Gln Glu Val
	325	330
Leu Ala Cys Gly Arg	Pro Gln Ala Thr Ala	Val Tyr Lys Val Ser Glu
	340	345
Tyr Ala Arg Arg Phe	Gly Val Pro Val Ile Ala	Asp Gly Gly Ile Gln
	355	360
Asn Val Gly His Ile	Ala Lys Ala Leu Ala Leu	Gly Ala Ser Thr Val
	370	375
Met Met Gly Ser Leu	Leu Ala Ala Thr Thr	Glu Ala Pro Gly Glu Tyr
385	390	395
Phe Phe Ser Asp Gly	Ile Arg Leu Lys Lys	Tyr Arg Gly Met Gly Ser
	405	410
Leu Asp Ala Met Asp	Lys His Leu Ser Ser	Gln Asn Arg Tyr Phe Ser
	420	425
Glu Ala Asp Lys Ile	Lys Val Ala Gln Gly	Val Ser Gly Ala Val Gln
	435	440
Asp Lys Gly Ser Ile	His Lys Phe Val Pro	Tyr Leu Ile Ala Gly Ile
450	455	460
Gln His Ser Cys Gln	Asp Ile Gly Ala Lys	Ser Leu Thr Gln Val Arg
465	470	475
Ala Met Thr Tyr Ser	Gly Glu Leu Lys Phe	Glu Lys Arg Thr Ser Ser
	485	490
Ala Gln Val Glu Gly	Gly Val His Ser Leu	His Ser Tyr Glu Lys Arg
	500	505
Leu Phe		510

<210> 31
 <211> 1707
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (67)...(1611)
 <223> mouse IMP dehydrogenase cDNA double mutant:
 Thr333Ile
 Ser351Tyr

<221> mutation
 <222> 1064
 <223> C to T mutation

<221> mutation
 <222> 1118
 <223> C to A mutation

<400> 31	
cctctgcggc gcggtcctcg gagcggcgcg gttctcggag ccacgcgtct gtcttcctcc	60
gtgggtc atg gcg gac tac ctg att agc gga ggc acc tct tac gtg ccg	108
Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro	
1 5 10	
gac gac ggg ctc aca gcg cag cag ctc ttc aac tgc ggg gac ggc ctc	156
Asp Asp Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu	
15 20 25 30	
acc tac aat gat ttt ctc att ctt cct ggg tat atc gac ttc act gca	204
Thr Tyr Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala	
35 40 45	
gat cag gtg gac ttg acg tct gct cta act aag aag att aca cta aag	252

Asp	Gln	Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys	
			50					55					60			
acc	cca	ttg	gtt	tcc	tca	ccc	atg	gac	act	gtc	aca	gag	gct	gga	atg	300
Thr	Pro	Leu	Val	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	
		65					70					75				
gcc	atc	gcg	atg	gcg	ctt	aca	gga	ggt	att	ggt	ttc	atc	cac	cac	aac	348
Ala	Ile	Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	
	80					85					90					
tgc	aca	cct	gaa	ttc	cag	gcc	aat	gaa	gtt	cgg	aaa	gtg	aag	aaa	tac	396
Cys	Thr	Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	
	95				100					105					110	
gaa	cag	gga	ttc	atc	act	gac	ccc	gtg	gtc	ctt	agc	ccc	aag	gat	cgt	444
Glu	Gln	Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	
				115					120					125		
gta	cgc	gat	gtt	ttt	gag	gcc	aaa	gcc	agg	cat	ggc	ttc	tgt	ggt	atc	492
Val	Arg	Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	
			130					135					140			
ccc	atc	aca	gat	aca	ggc	cgg	atg	ggg	agt	cga	ttg	gtg	ggc	atc	atc	540
Pro	Ile	Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	
		145					150					155				
tcc	tca	agg	gac	att	gat	ttc	ctc	aag	gag	gaa	gag	cat	gac	cgg	ttc	588
Ser	Ser	Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Arg	Phe	
	160					165					170					
ttg	gaa	gag	atc	atg	act	aag	agg	gaa	gat	ttg	gtg	gtc	gcc	cct	gcc	636
Leu	Glu	Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Ala	
	175				180					185					190	
ggc	gtc	act	ctg	aaa	gag	gca	aat	gag	att	ctg	cag	cga	agt	aaa	aag	684
Gly	Val	Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	
				195				200						205		
gga	aag	ttg	ccc	att	gtg	aat	gaa	aat	gat	gag	ctg	gta	gcc	atc	att	732
Gly	Lys	Leu	Pro	Ile	Val	Asn	Glu	Asn	Asp	Glu	Leu	Val	Ala	Ile	Ile	
			210					215					220			
gcc	cgg	aca	gac	cta	aag	aag	aat	cgt	gat	tac	ccc	ctg	gcc	tcc	aaa	780
Ala	Arg	Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	
		225					230					235				
gat	gcc	aag	aag	caa	ctg	ctg	tgt	ggg	gca	gcc	att	ggc	act	cat	gag	828
Asp	Ala	Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	
	240				245						250					
gat	gac	aag	tat	agg	ctg	gac	tta	ctg	gcc	ctt	gct	ggg	gtg	gat	gta	876
Asp	Asp	Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Leu	Ala	Gly	Val	Asp	Val	
	255				260				265						270	
gtg	gtt	ttg	gac	tct	tcc	cag	gga	aac	tcc	atc	ttc	caa	atc	aat	atg	924
Val	Val	Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	
				275					280					285		
atc	aaa	tac	atc	aag	gag	aag	tat	ccc	agt	cta	cag	gtc	att	gga	ggc	972
Ile	Lys	Tyr	Ile	Lys	Glu	Lys	Tyr	Pro	Ser	Leu	Gln	Val	Ile	Gly	Gly	
			290					295					300			
aat	gta	gtc	act	gct	gcg	caa	gcc	aag	aac	ctc	ata	gat	gca	ggt	gta	1020
Asn	Val	Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	

305					310					315						
gat	gct	ttg	cga	gtc	ggc	atg	gga	agt	ggt	tcc	atc	tgc	atc	atc	cag	1068
Asp	Ala	Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Ile	Gln	
	320					325					330					
gaa	gtg	ttg	gcc	tgt	ggg	cgg	ccc	caa	gcc	aca	gca	gtg	tac	aag	gtc	1116
Glu	Val	Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	
	335				340					345					350	
tat	gag	tat	gcc	cgt	cgc	ttt	ggt	gtt	cct	gtt	att	gct	gat	gga	gga	1164
Tyr	Glu	Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	
				355					360					365		
atc	caa	aat	gtg	ggt	cat	att	gcc	aaa	gct	ttg	gct	ctt	ggg	gct	tcc	1212
Ile	Gln	Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	
			370					375					380			
aca	gtc	atg	atg	ggc	tcc	ctc	ctg	gct	gcc	acc	act	gag	gcc	cct	ggc	1260
Thr	Val	Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	
		385					390					395				
gag	tac	ttc	ttc	tca	gat	ggg	atc	cgg	ctg	aag	aaa	tac	cga	ggt	atg	1308
Glu	Tyr	Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	
	400					405					410					
ggt	tct	ctt	gat	gcc	atg	gac	aaa	cat	ctc	agc	agc	cag	aac	cga	tac	1356
Gly	Ser	Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	
	415				420					425					430	
ttc	agt	gaa	gct	gac	aaa	atc	aaa	gtg	gcc	caa	gga	gtt	tca	ggg	gca	1404
Phe	Ser	Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	
				435					440					445		
gtg	cag	gac	aag	ggg	tct	atc	cac	aag	ttc	gtt	cct	tac	ctg	att	gct	1452
Val	Gln	Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	
			450					455					460			
ggc	atc	cag	cat	tcc	tgt	caa	gac	att	ggt	gcc	aag	agt	tta	acc	caa	1500
Gly	Ile	Gln	His	Ser	Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	
		465					470					475				
gtc	aga	gcc	atg	acg	tac	tcg	ggg	gag	ctt	aaa	ttt	gag	aag	agg	aca	1548
Val	Arg	Ala	Met	Thr	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	
	480					485					490					
tcc	tct	gct	cag	gtg	gaa	ggt	ggc	gtc	cac	agc	ctc	cat	tcg	tac	gag	1596
Ser	Ser	Ala	Gln	Val	Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	
	495				500					505					510	
aaa	cgg	ctt	ttc	tga	aaacagatcc	agtatatgcc	ttgaattttt	caataaaagt								1651
Lys	Arg	Leu	Phe	*												
ttgggaaaaa	aaaagtgaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1707
<210>	32															
<211>	514															
<212>	PRT															
<213>	Mus musculus															
<400>	32															
Met	Ala	Asp	Tyr	Leu	Ile	Ser	Gly	Gly	Thr	Ser	Tyr	Val	Pro	Asp	Asp	
1				5					10					15		
Gly	Leu	Thr	Ala	Gln	Gln	Leu	Phe	Asn	Cys	Gly	Asp	Gly	Leu	Thr	Tyr	

Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Tyr	Ile	Asp	Phe	Thr	Ala	Asp	Gln
		35					40					45			
Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys	Thr	Pro
	50					55					60				
Leu	Val	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	Ala	Ile
65					70					75					80
Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr
				85					90					95	
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln
			100					105					110		
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg
		115					120					125			
Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile
	130					135					140				
Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser
145					150					155					160
Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Arg	Phe	Leu	Glu
				165					170					175	
Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Ala	Gly	Val
			180					185					190		
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys
		195					200					205			
Leu	Pro	Ile	Val	Asn	Glu	Asn	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg
	210					215					220				
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala
225					230					235					240
Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp
				245					250					255	
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Leu	Ala	Gly	Val	Asp	Val	Val	Val
			260					265					270		
Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys
		275					280					285			
Tyr	Ile	Lys	Glu	Lys	Tyr	Pro	Ser	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val
	290					295					300				
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala
305					310					315					320
Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Ile	Gln	Glu	Val
				325					330					335	
Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Tyr	Glu
			340					345					350		
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln
		355					360					365			
Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val
	370					375					380				
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr
385					390					395					400
Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser
				405					410					415	
Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser
			420					425					430		
Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln
		435					440					445			
Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile
	450					455					460				
Gln	His	Ser	Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg
465					470					475					480
Ala	Met	Thr	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser
				485					490					495	
Ala	Gln	Val	Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg
			500					505					510		

<210> 33
<211> 5627

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of pMG
plasmid from InvivoGen

<400> 33

caccggcgaa	ggaggcctag	atctatcgat	tgtacagcta	gctcgacatg	ataagataca	60
ttgatgagtt	tggacaaacc	acaactagaa	tgcagtga	aaaatgcttt	atttgtgaaa	120
tttgtgatgc	tattgcttta	tttgtgaaat	ttgtgatgct	attgctttat	ttgtaaccat	180
tataagctgc	aataaacaag	ttaacaacaa	caattgcatt	cattttatgt	ttcaggttca	240
gggggaggtg	tgggaggttt	tttaaagcaa	gtaaaacctc	tacaaatgtg	gtagatccat	300
ttaaatgtta	attaagaaca	tgtgagcaaa	aggccagcaa	aaggccagga	accgtaaaaa	360
ggccgcgttg	ctggcgTTTT	tccataggct	ccgccccct	gacgagcatc	acaaaaatcg	420
acgctcaagt	cagaggtggc	gaaacccgac	aggactataa	agataccagg	cgtttcccc	480
tggaagctcc	ctcgtgcgct	ctcctgttcc	gaccctgccg	cttaccggat	acctgtccgc	540
ctttctccct	tccggaagcg	tggcgctttc	tcatagctca	cgctgtaggt	atctcagttc	600
ggtgtaggtc	gttcgctcca	agctgggctg	tgtgcacgaa	cccccggttc	agcccgaccg	660
ctgcgcctta	tccggttaact	atcgtcttga	gtccaacccg	gtaagacacg	acttatcgcc	720
actggcagca	gccactggta	acaggattag	cagagcgagg	tatgtaggcg	gtgctacaga	780
gttcttgaag	tggtaggcta	actacggcta	cactagaaga	acagtatttg	gtatctgcgc	840
tctgctgaag	ccagttacct	tccgaaaaag	agttggtagc	tcttgatccg	gcaaacaaac	900
caccgctggg	agcggtggtt	tttttgtttg	caagcagcag	attacgcgca	gaaaaaaagg	960
atctcaagaa	gaccccttga	tcttttctac	ggggtctgac	gctcagtggg	acgaaaactc	1020
acgttaaggg	attttgggtc	tggctagtta	attaagctgc	aataaacaat	cattattttc	1080
attggatctg	tgtgttggtt	ttttgtgtgg	gcttggggga	gggggaggcc	agaatgactc	1140
caagagctac	aggaaggcag	gtcagagacc	ccactggaca	aacagtggct	ggactctgca	1200
ccataacaca	caatcaacag	gggagtga	tggatcgagc	tagagtcctg	tacataactt	1260
acggtaaatg	gcccgcctgg	ctgaccgccc	aacgaccccc	gcccattgac	gtcaataatg	1320
acgtatgttc	ccatagtaac	gccaataggg	actttccatt	gacgtcaatg	ggtggagtat	1380
ttacggtaaa	ctgcccactt	ggcagtagat	caagtgtatc	atatgccaa	tacgccccct	1440
attgacgtca	atgacggtaa	atggcccgc	tggcattatg	cccagtagat	gaccttatgg	1500
gactttccta	cttggcagta	catctacgta	ttagtcatcg	ctattaccat	ggtgatgcgg	1560
ttttggcagt	acatcaatgg	gcgtggatag	cggtttgact	cacggggatt	tccaagtctc	1620
caccccatgg	acgtcaatgg	gagtttgttt	tggcaccaaa	atcaacggga	ctttccaaaa	1680
tgtcgtaaca	actccgcccc	attgacgcaa	atgggcggta	ggcgtgtacg	gtgggaggtc	1740
tataataagc	gagctcgttt	agtgaaccgt	cagatcgctt	ggagacgcca	tccacgctgt	1800
tttgacctcc	atagaagaca	ccgggaccga	tccagcctcc	gcgggccggg	acggtgcatt	1860
ggaacgcgga	ttccccgtgc	caagagtga	gtaagtaccg	cctatagagt	ctataggccc	1920
accccccttg	cttcttatgc	atgctatact	gtttttggct	tggggcttat	acacccccgc	1980
ttcctcatgt	tataggtgat	ggtatagctt	agcctatagg	tgtgggttat	tgaccattat	2040
tgaccactcc	cctattgggtg	acgatacttt	ccattactaa	tccataacat	ggctcctttg	2100
cacaactctc	tttattggct	atatgccaat	acactgtcct	tcagagactg	acacggactc	2160
tgtattttta	caggatgggg	tctcatttat	tatttataaa	ttcacatata	caacaccacc	2220
gtccccagtg	cccgaggttt	ttattaaaca	taacgtggga	tctccacgcg	aatctcgggt	2280
acgtgttccg	gacatgggct	cttctccggt	agcggcggag	cttctacatc	cgagccctgc	2340
tcccatgcct	ccagcgactc	atggctcgct	ggcagctcct	tgctcctaac	agtggaggcc	2400
agacttaggc	acagcacgat	gcccaccacc	accagtgtgc	cgcacaaggc	cgtggcggtg	2460
gggtatgtgt	ctgaaaatga	gctcggggag	cgggcttgca	ccgctgacgc	atttgggaag	2520
cttaaggcag	cggcagaaga	agatgcaggc	agctgagttg	ttgtgttctg	ataagagtca	2580
gaggtaactc	ccgttgcggt	gctgttaacg	gtggagggca	gtgtagtctg	agcagtactc	2640
gttgctgccg	cgcgcgccac	cagacataat	agctgacaga	ctaacagact	gttcctttcc	2700
atgggtcttt	tctgcagtca	cccgggggat	ccttcgaacg	tagctctaga	ttgagtcgac	2760
gttactggcc	gaagccgctt	ggaataaggc	cggtgtgcgt	ttgtctatat	gttattttcc	2820
accatattgc	cgtcttttgg	caatgtgagg	gcccggaaac	ctggccctgt	cttcttgacg	2880
agcattccta	ggggctcttt	ccctctcgcc	aaaggaatgc	aaggtctgtt	gaatgtcgtg	2940
aaggaagcag	ttcctctgga	agcttcttga	agacaaacaa	cgtctgtagc	gaccctttgc	3000
aggcagcgga	acccccacc	tggcgacagg	tgcctctgcg	gccaaaagcc	acgtgtataa	3060
gatacacctg	caaaggcggc	acaaccccag	tgccacgttg	tgagttggat	agttgtggaa	3120
agagtcaaat	ggctctctc	aagcgtatct	aacaaggggc	tgaaggatgc	ccagaaggta	3180
ccccattgta	tgggatctga	tctggggcct	cggtgcacat	gctttacatg	tgtttagtcg	3240
aggttaaaaa	aacgtctagg	ccccccgaac	cacggggacg	tgggttttcc	ttgaaaaaca	3300
cgataatacc	atgggttaagt	gatatctact	agttgtgacc	ggcgcttagt	gttgacaatt	3360
aatcatcggc	atagtatatc	ggcatagtat	aatacgactc	actataggag	ggccaccatg	3420

```

tcgactacta accttcttct ctttcctaca gctgagatca ccggtaggag ggccatcatg 3480
aaaaagcctg aactcaccgc gacgtctgtc gcgaagtttc tgatcgaaaa gttcgacagc 3540
gtctccgacc tgatgcagct ctccggagggc gaagaatctc gtgctttcag cttcgatgta 3600
ggagggcgctg gatatgtcct gcgggttaa atgctgcgcg atggttttcta caaagatcgt 3660
tatgtttatc ggcacttttg atcggccgcg ctcccgattc cggaagtgtc tgacattggg 3720
gaattcagcg agagcctgac ctattgcac tcccgcctg cacaggggtg cacgttgcaa 3780
gacctgcctg aaaccgaact gcccgctgtt ctgcaaccgc tcgcggagct catggatgcg 3840
atcgctgcgg ccgatcttag ccagacgagc gggttcggcc cattcggacc gcaaggaatc 3900
ggtcaataca ctacatggcg tgatttcata tgcgcgattg ctgatcccca tgtgtatcac 3960
tggcaaactg tgatggacga caccgtcagt gcgtccgtcg cgcaggctct cgatgagctg 4020
atgctttggg ccgaggactg ccccgaagtc cggcacctcg tgcacgcgga tttcggctcc 4080
aacaatgtcc tgacggacaa tggccgcata acagcgggtc ttgactggag cgaggcgatg 4140
ttcgggggatt cccaatacga ggtcgccaac atcttcttct ggaggccgtg gttggcttgt 4200
atggagcagc agacgcgcta cttcgagcgg aggcattccg agcttgcagg atcgccgcgg 4260
ctccgggcgt atatgtccg cattggtctt gaccaactct atcagagctt ggttgacggc 4320
aatttcgatg atgcagcttg ggcgcagggc cgatgcgacg caatcgctcg atccggagcc 4380
gggactgtcg ggcgtacaca aatcgccgcg agaagcgcg ccgtctggac cgatggctgt 4440
gtagaagtac tcgccgatag tggaaaccga cgccccagca ctgctccgag ggcaaaggaa 4500
tgagtcgaga attcgctaga gggccctatt ctatagtgtc acctaaatgc tagagctcgc 4560
tgatcagcct cgactgtgcc ttctagtgtc cagccatctg ttgtttgccc ctcccccggtg 4620
cttcccttga cctcggaagg tgcctctccc actgtccttt cctaataaaa tgaggaaatt 4680
gcatcgcatt gtctgagtag gtgtcattct attctggggg gtgggggtgg gcaggacagc 4740
aagggggagg attgggaaga caatagcagg catgcgcagg gcccaattgc tcgagcggcc 4800
gcaataaaa atctttatct tcatcacatc tgtgtgttgg ttttttgtgt gaatcgtaac 4860
taacatacgc tctccatcaa aacaaaacga aacaaaacaa actagcaaaa taggctgtcc 4920
ccagtgcag tgacaggtgcc agaacatttc tctatcgaag gatctgcgat cgctccgggtg 4980
cccgctcagt ggcagagcgc acatcgccca cagtccccga gaagtggggg ggaggggtcg 5040
gcaattgaac cgggtgcctag agaaggtggc gcggggtaaa ctgggaaagt gatgtcgtgt 5100
actggctccg cttttttccc gaggggtggg gagaaccgta tataagtgca gtagtcgccg 5160
tgaacgttct ttttcgcaac gggtttgccg ccagaacaca gctgaagctt cgaggggctc 5220
gcatctctcc ttcacgcgcc cgccgcctta cctgaggccg ccatccacgc cggttgagtc 5280
gcgttctgcc gcctcccgcc tgtggtgct cctgaactgc gtccgcctgc taggtaagtt 5340
taaagctcag gtcgagaccg ggcctttgtc cggcgctccc ttggagccta cctagactca 5400
gccggctctc cacgcttttg ctgaccctgc ttgctcaact ctacgtcttt gtttcgtttt 5460
ctgttctgcg ccgttacaga tccaagctgt gaccggcgcc tacgtaagtg atatctacta 5520
gatttatcaa aaagagtgtt gacttgtgag cgctcacaat tgatacttag attcatcgag 5580
agggacacgt cgactactaa ccttcttctc tttcctacag ctgagat 5627

```

<210> 34
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Forward primer for amplification-based cloning of hIMPDH type II cDNA

<400> 34
 gctatctgca ggccgccacc atggccgact acctgattag 40

<210> 35
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Reverse primer for amplification-based cloning of hIMPDH type II cDNA

<400> 35
 catactcttc gccgaaaaga ctgatctcg atc 33

<210> 36

<211> 32
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Forward primer for T333I mutation of hIMPDH type II cDNA

<400> 36
ggctccatct gcattatcca ggaagtgctg gc

32

<210> 37
<211> 32
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reverse primer for T333I mutation of hIMPDH type II cDNA

<400> 37
ccgaggtaga cgtaataggt ccttcacgac cg

32

<210> 38
<211> 38
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Forward primer for S351Y mutation of hIMPDH type II cDNA

<400> 38
cagcagtgtgta caaggtgtat gagtatgcac ggcgcttt

38

<210> 39
<211> 39
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reverse primer for S351Y mutation of hIMPDH type II cDNA

<400> 39
gtcgtcacat gttccacata ctcatacgtg ccgcgaaac

39